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ALIGNMENTS

RESULT 1 07-SEP-2001 Human IL-20 receptor subunit IL-20RA extracellular domain fragment AAB85269 standard; (first protein; entry) 221 ₿

dermatological; antiinflammatory; Interleukin 20; IL-20; IL-20RA; ZcytoR7; IL-20RB; DIRS1; immunoglobulin; antiulcer; antipsoriatic; antiasthmatic; antibacterial; human; antagonist.

Homo sapiens.

WO200146232-A2

28-JUN-2001.

22-DEC-2000; 2000WO-US035307.

23-DEC-1999; 99US-00471774 22-JUN-2000; 2000US-0213416P

(ZYMO) ZYMOGENETICS INC.

Rixon MW, Foster DC, Presnell Xu W, Madden SR, Fox BA; 3 Kelly JD, Sprecher CA, Brandt CS;

WPI; 2001-398320/42.

Isolated interleukin 20 soluble receptor comprising two polypeptide subunits IL-20RA and IL-20RB, useful for down-regulating IL-20 and thus treating inflammatory diseases such as psoriasis.

Claim 1; Page 65; 119pp; English.

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OS Hom comprising two polypeptide subunits IL-20RA (formerly known as ZcytoR7) and IL-20RB (formerly known as DIRS1). The two subunits are preferably linked together. In one embodiment, one subunit is fused to the constant region of the light chain of an immunoglobulin, and the other subunit is fused to constant region of the heavy chain of an immunoglobulin. The light chain and the heavy chain are connected via a disulphide bond. The soluble receptor can be used to down-regulate IL-20 and thus treat inflammatory diseases such as psoriasis, inflammatory lung injury such as The invention relates to an interleukin 20 (IL-20) soluble receptor or bronchitis, adult respiratory disease (ARD), septic ae

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RESULT 2

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(CHAN/)
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(BLUM/)
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                                                                                                                                                                                                                                                                   (FOST/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       reperfusion injury; cancer; meningitis; rheumatic disease; skin disease; idiopathic pulmonary fibrosis; inflammatory bowel disease; psoriasis; ulcerative colitis; eczema; atopic dermatitis; contact dermatitis; inflammatory lung disease; ARD; adult respiratory disease; asthma;
                                                                                                                                                                                                                                                                                                                                        22-JUN-2000; 2000US-0213341P
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) MADDEN K L.

) KELLY J D.

SERECHER C A.

) SPIMBERG H.
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The invention describes a method (I) for treating a mammal afflicted with a disease in which an interleukin-20 (II-20) polypeptide plays a role comprising administering antagonist of the II-20 polypeptide to the CC comprising administering antagonist of the II-20 polypeptide to the CC comprising administering antagonist of the III-20 polypeptide to the CC comprising administering tytokine in the inflammatory process is CC via chemotaxis and the release of granule enzymes. II-8 binds to CC via chemotaxis and the release of granule enzymes. II-8 binds to CC periodontal disease are characterised by the influx of neutrophils. II-8 is a potent inducer of angiogenesis in several angiogenesis-dependent chronic inflammatory conditions, including rheumatoid arthritis, is an cimportant source of angiogenic activity in human lung cancer. Also, II-8 is an CC important source of angiogenic activity in human lung cancer. Also, II-8 cxpression correlates with experimental metastatic activity of some melanoma cell lines. Therefore an effective method to treat inflammatory diseases would be to administer an agent that would inhibit II-8. It has been shown that II-20 up-regulates II-8. Therefore antagonists to II-20 can be used to treat these diseases. The method is used for treating cinjury, cancer, meningitis, rheumatic diseases, idiopathic pulmonary fibrosis, cataracts, reperfusion can fibrosis, inflammatory bowel disease (lacerative colitis), skin disease (ground states) and contact dermatitis) or an activity and pneumonia). This sequence represents a human interleukin-cc 20 (II-20) polypeptide used in developing the method of the invention
  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Treating inflammatory skin and lung diseases using antibodies against interleukins (IL)-20 (which indirectly modulates activation of IL-8), useful for treating e.g. psoriasis, asthma and bronchitis.
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AA;
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               PNTLYCVHVESFVPGPPRRAQPSEKQCARTLKDQSSEFKAK
                                          SISVVLTAPEKWKRNPEDLPVSMQQIYSNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLE
                                                      SISVVLTAPEKWKRNPEDLPVSMQQIYSNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLE
                                                                                                                                                 VPCVSGGLPKPANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYFIYGQKKWLNKSECRN
PNTLYCVHVESFVPGPPRRAQPSEKQCARTLKDQSSEFKAK
                                                                                     INRTYCDLSAETSDYEHQYYAKVKAIWGTKCSKWAESGRFYPFLETQIGPPEVALTTDEK
                                                                                                           INRTYCDLSAETSDYEHQYYAKVKAIWGTKCSKWAESGRFYPFLETQIGPPEVALTTDEK
                                                                                                                                 VPCVSGGLPKPANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYFIYGQKKWLNKSECKN
                                                                                                                                                                                  Conservative
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KW Linte
KW diak
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                                                                    standard;
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Human IL-20RA mature extracellular protein.

Human; interleukin-19; IL-19; interleukin-20 receptor alpha; IL-20RA; interleukin-20 receptor beta; IL-20RB; inflammation; atherosclerosis; diabetes; reperfusion injury; cancer; infectious meningitis; cataract

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           inflammation; single chain antibody; interleukin; IL-20; IL-20RA IL-20RB subunit; antiinflammatory; dermatological; antipsoriatic; antiarthritic; respiratory; antiasthmatic; antiulcer; antibacteri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI;
                                                                    Human
                                                                                                                                                ADJ83292 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rheumatoid arthritis; rheumatic fever; systemic lupus erythematosus; antibacterial; cytostatic; dermatological; ophthalmological; vasotropic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Method
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                                       inflammation;
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                                                                                                                                                                                                                   PNTLYCVHVESFVPGPPRRAQPSEKQCARTLKDQSSEFKAK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  down-regulating IL-19 useful for treating inflammation administration of a polypeptide comprised of the extracellular IL-20RA and IL-20RB.
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                                                                 subunit extracellular domain
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100.0%; Pr
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SISVVLTAPEKWKRNPEDLPVSMQQIYSNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLE

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INRTYCDLSAETSDYEHQYYAKVKAIWGTKCSKWAESGRPYPFLETQIGPPEVALTTDEK

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Query Match
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22-JUN-2000;
22-DEC-2000;
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Blumberg
                                                                                                                                                                                                                         antilicer, antibacterial, immunosuppressive and gastrointestinal applications and may be useful for reducing or treating an inflammation, including an inflammatory skin disease such as psoriasis, eczema, atopic dermatitis and contact dermatitis or an inflammatory lung disease such as adult respiratory distress syndrome, asthma, bronchitis and pneumonia, as well as arthritis, septic shock, multiple organ failure, inflammatory bowel disease, ulcerative colitis or Crohn's disease. The current
                                                                                                                                                                                                                                                                                                                                                  inflammation in a mammal which comprises administering an antibody, antibody fragment or single chain antibody which specifically binds to a receptor of interleukin (IL)-20 comprising an IL-20RA subunit and an IL-20RB subunit. The method of the invention has antiinflammatory, dermatological, antiporiatic, antiarthritic, respiratory, antiasthmatic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Reducing or treating inflammation, e.g. inflammatory lung disease, comprises administering an antibody, antibody fragment or single chain antibody that specifically binds to an interleukin (IL)-20RA subunit o
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adult respiratory distress syndrome; asthma; bronchitis
arthritis; septic shock; multiple organ failure; bowel;
ulcerative colitis; Crohn's disease; human; receptor;
                                                                                                                                                  Sequence
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(XUWW/)
(MADD/)
                                                                                                                                                                                                         sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO
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(CHAN/)
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SPRECHER C A.
BLUMBERG H.
BAGAN M A.
CAGAN B R.
JASPERS S R.
CHANDRASEKHER '
NOVAK J E.
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Jaspers
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Pred. No. 3
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                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Treating or preventing inflammation, immune system, cardiovascular and hematopoietic disorders, and regulation of cellular proliferation comprises administering proteins inhibiting cytokine signaling, e.g.
                                                                                                                                                                                                                                                                                                                                                                           Sequence
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DB; ACC58076.
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                               INRTYCOLSAETSDYEHQYYAKVKAIWGTKCSKWAESGRFYPFLETQIGPPEVALTTDEK
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                                                                                                                                                                                                                                                        Score 1200; DB 6;
Pred. No. 3.3e-112;
; Mismatches 0;
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RESULT 6
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ADUI 265
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Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte. A-peptide; factor VIIA; gene therapy.
                                                                                                                                                    Human PRO4978 polypeptide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SISVVLTAPEKWKRNPEDLPVSMQQIYSNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PNTLYCVHVESFVPGPPRRAQPSEKQCARTLKDQSSEFKAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PNTLYCVHVESFVPGPPRRAQPSEKQCARTLKDQSSEFKAK 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SISVVLTAPEKWKRNPEDLPVSMQQIYSNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLE
                                                                                                                                                                                                                                                                                                                                        542 AA.
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RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local (
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Smith V,
PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNP-alpha; blood; chondrocyte cell; cell proliferation; cell differentiation; colon; adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated, secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bioactive molecules to cells expressing polypeptides, and detect the presence of mammalian tumors e.g. lung,
                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU29222
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                                                                                                                                                                                                                                                                                                                                                                                                                             standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SISVVLTAPEKWKRNPEDLPVSMQQIYSNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLE
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                                                                                                                                                                                            polypeptide
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E, Goddard
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                                                                                                                                                                                                                                                                                                                                                                                                                             protein; 542
                                                                                                                                                                                                                                                                        entry)
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Tumas
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A, Godowski PJ, Gurney AL, Sh
Tumas D, Watanabe CK, Wood WI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
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Pred. No. 1.2e-111;
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L, Sherwood
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Baker Pan J, KP, Chen J Ģ , Desnoyers Watanabe CK, ۲ Wood WI, A, Go Zhang Godowski Ŋ Ę, Gurney ΑL;

N-PSDB; 2001-602746/68. AAS46123.

Novel nucleic acids encoding PRO polypeptides, used to presence of tumors, such as prostate and breast tumors, screen for modulators of the compounds. diagnose the the and ç

Claim 11; Fig 398; 774pp; English.

Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention. The PRO polypeptides and their associated nucleic acids can be used to detect the presence of a tumour in a mammal by comparing the level of expression of a PRO polypeptide in a test sample of cells from the anima and a control sample of normal cells, whereby a higher level of expression in the test sample indicates the presence of a tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats and rabbits but are preferably human. The polypeptides can be used to stimulate tumour necrosis factor (TNF) alpha release from human blood, when contacted with it. A specific polypeptide can be used to stimulate animal

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ow; horse; sheep; pig; goat; rabbit; ADEPT;
pendent enzyme mediated prodrug therapy.
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tissue
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S-0101786P.
S-0102207P.
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S-010231P.
S-010231P.
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S-0102571P.
 S-0059263P.
S-0063256P.
S-0063486P.
S-0063121P.
S-0063121P.
S-0063141P.
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3-0089512P. 3-0089514P. 3-0089538P. 3-0089598P.

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RESULT 11
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                                                                                                                                                                                                                             Human; PRO; secreted protein; transmembrane protein; extracellular domain; tumour necrosis factor-alpha; TNF-alpha; extracellular domain; tumour necrosis factor-alpha; TNF-alpha; chondrocyte; proliferation; differentiation; cartilage disorder; bone disorder; arthritis; sports injury; cancer; tumour; diagnosis; adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cerv: liver; drug screening; transgenic animal; genetic analysis; antiarthritic; vulnerary; gene therapy.
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Similarity 100.0%; P
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16-JUN-1998;
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98US-0089538P 98US-008953P 98US-009904P 98US-009904P 98US-0099041P 98US-0099041P 98US-0099041P 98US-0099053P 98US-0099051P 98US-0099054P 98US-0099054P 98US-0099054P 98US-0099059P 98US-0099059P 98US-0099059P 98US-0091010P 98US-0091544P 98US-0091544P 98US-0091544P 98US-0091544P 98US-009154P 98US-009152P 98US-009168P 98US-009168P 98US-009169P 98US-009169P 98US-009169P 98US-009168P 98US-009168P 98US-009168P 98US-009169P 98US-009168P 98US-009168P

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RESULT 12
ABR65725
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Best Local Sim
Matches 221;
                                                                                                 Human; PRO; secreted protein; transmembrane protein; extracellular domain; tumour necrosis factor-alpha; TNP-alpha; chondrocyte; proliferation; differentiation; cartilage disorder; bone disorder; arthritis; sports injury; cancer; tumour; diagnosis; adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cerv; liver; drug screening; transgenic animal; genetic analysis; antiarthritic; vulnerary; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-SEP-1998
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                                              US2003036159-A1.
                                                                                                                                                                                                                                             Human
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21; Conservative
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98US-0100684P.
98US-0100919P.
98US-01001014P.
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Pred. No. 1.2e-111;
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97US-0059263P

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05-JUN-1998; 09-JUN-1998; 10-JUN-1998; 10-JUN-1998;

3-0088217P. 3-0088655P. 3-0088722P. 3-0088738P.

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RESULT 13
ABU99665
ID ABU9965
XX ABU996
XX ABU99
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                                       Human;
tumour
tissue
                                                                        Human
         US2003040070-A1
                         Homo sapiens.
                                                                                        09-AUG-2003
                                                                                                          ABU99665;
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Similarity 100.0%;
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                                                                                                                                                                PNTLYCVHVESFVPGPPRRAQPSEKQCARTLKDQSSEFKAK
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                                                                                                                         standard;
                                                                                         (first
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98US-0099763P.
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98US-0102570P.
98US-0102570P.
98US-0102584P.
98US-01025684P.
                                                 and transmembrane protein; PRO;
factor alpha; chondrocyte cell;
                                                                                                                        protein;
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Pred. No. 1.2e-111;
; Mismatches 0;
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                                              TNF-alpha;
tumour; gene therapy;
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98US-008025E. 98US-0087098P. 98US-0087208P. 98US-0087609P. 98US-0087877P. 98US-0088025P. 98US-0088023P. 98US-0088023P. 98US-0088025P. 98US-0088025P. 98US-0088025P. 98US-0088025P.	97US-005256P 97US-005926AP 97US-005926AP 97US-0063120P 97US-0063121P 97US-006354AP 97US-006354AP 97US-0063511P 97US-0063112P 97US-0063111P 97US-006311P 97US-0066120P 97US-0066120P 97US-0066120P 97US-006646AP 97US-00669335P 97US-0069335P 97US-0069335P 97US-0069370P 98US-0077464P 98US-0077632P 98US-007764P 98US-007976P 98US-007976P 98US-008107P 98US-008107P 98US-0081195P 98US-0081195P 98US-0081195P 98US-0081195P 98US-0081332P 98US-008332P 98US-008345AP 98US-008345AP 98US-008345P 98US-008345P 98US-008444AP 98US-008463P 98US-008463P 98US-008463P 98US-008455P 98US-008455P 98US-008455P 98US-008455P 98US-008455P 98US-008455P 98US-008455P 98US-008455P 98US-008455P 98US-008455P 98US-00855P 98US-00855P 98US-00855P 98US-00855P 98US-00855P 98US-00855P 98US-00855P	
		
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RESULT 14
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Best Local Sim
Matches 221;
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116-SEP-1998
116-SEP-1998
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                  Human; PRO chromosome
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Similarity 100,
21; Conservative
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                                                                                                                                                            standard;
                                                                                                                                                                                                                                        PNTLYCVHVESFVPGPPRRAQPSEKQCARTLKDQSSEFKAK
                                                                                                                                                                                                                                                              PNTLYCVHVESFVPGPPRRAQPSEKQCARTLKDQSSEFKAK
                                                             polypeptide #199.
              polypeptide; secreted and transmembrane protein; tumour; mapping; gene mapping; cytostatic.
                                                                                              (first
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98US-0099754P
98US-0099763P
98US-0100664P
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98US-0100683P
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                                                                                                                                                          protein;
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Pred. No. 1.2
D; Mismatches
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97US-0059263P-
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97US-0063486P-
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98US-0081097-
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RESULT 15
ABO17709
ID ABO17
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Pred. No. 1.2e-111;
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04-JUN-1998;
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98US-008803P98US-008815P98US-008815P98US-008815P98US-008821P98US-008821P98US-008821P98US-008881P98US-008881P98US-008881P98US-008881P98US-008882P98US-0088953P98US-008953P98US-008953P98US-008953P98US-0090754P98US-0090754P98US-0090754P98US-0090754P98US-0090754P98US-0090754P98US-0090754P98US-0090754P98US-0090754P98US-0090757P98US-009163P98US-009163P98US-009163P98US-009163P98US-009163P98US-009163P98US-009163P98US-009163P98US-009163P98US-009163P98US-009163P98US-009163P98US-009163P98US-009163P98US-009163P98US-009163P98US-009163P98US-009163P98US-009163P98US-009173P98US-009773P98US-009773P98US-009773P98US-009773P98US-009773P98US-009773P98US-009773P98US-009773P98US-009773P-

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14-SEP-1998
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05-JAN-1999
10-MAR-1999
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11-SEP
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98WO-US022991

98WO-US022992

98WO-US024855

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99WO-US0050186

99WO-US010733

99WO-US010733

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102-MAR-2000
110-MAR-2000
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2000WO-US006319.
2000WO-US006884.
2000WO-US007377.
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Baker KP, Gerritsen Smith V, n ME, Goddard Stewart TA, Tumas Deforge L, Desnoyers L, Filva A, Godowski PJ, Gurney AL, Sh Numas D, Watanabe CK, Wood WI, Filvaroff E, Ga AL, Sherwood S; ood WI, Zhang Z; Gao Σ

WPI; N-PSDB; 2003-341980/32. DB; ACD23946.

syndrome New secreted and transmembrane PRO nucleic acids, for inflammation, organ failure, atherosclerosis, cardiac infertility, birth defects, premature aging, axquired syndrome (AIDS), or cancer. treating injury, immunodeficiency

Claim 12; Fig 188; 660pp; English.

The invention describes an isolated nucleic acid (I) comprising, or which has 80 % sequence identity to, or the full-length coding sequence of, on of 275 nucleotide sequences, and which encodes a corresponding polypeptide selected from 275 amino acid sequences, where all sequences are given in the specification. The polypeptide encoded by (I) is used to detect PRO polypeptides, link a bioactive molecule to a cell expressing after the polypeptide, modulate a biological activity of a cell, stimulate the release of tumour necrosis factor (TNF)-alpha from human blood, modulate 0f tumour necrosis factor (TNF)-alpha of glucose or free fatty acid by ce cells, stimulate 유 or which e of, one a to

밁 S 문 5 밁 Ş 밁 5 8888888888888888 Query Match 100.0%; Score 1200; DB 6; Best Local Similarity 100.0%; Pred. No. 1.2e-111; Matches 221; Conservative 0; Mismatches 0; the proliferation or differentiation of cells or gene expression, stimulate the release of proteoglycans, stimulate the release of cytokine from peripheral blood mononuclear cells, inhibit the binding of A-peptide to factor VIIA, or detect the presence of tumour in a mammal. The nucleic diseases, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, acquired immunodeficiency syndrome (AIDS), cancer, or diabetic complications. The nucleic acid is useful as hybridisation probes, in chromosome and gene mapping, and in generating antisense RNA or DNA. The polypeptides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. Both are useful in tissue typing. This is the amino acid sequence of a novel human secreted and Sequence 542 AA; 199 139 181 121 79 61 INRTYCDLSAETSDYEHQYYAKVKAIWGTKCSKWAESGRFYPFLETQIGPPEVALTTDEK 120 19 ш PNTLYCVHVESFVPGPPRRAQPSEKQCARTLKDQSSEFKAK 221 SISVVLTAPEKMKRNPEDLPVSMQQIYSNLKYNVSVLNTKSNRTMSQCVTNHTLVLTMLE 180 SISVVLTAPEKWKRNPEDLPVSMQQIYSNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLE INRTYCOLSAETSDYEHQYYAKVKAIWGTKCSKWAESGRFYPFLETQIGPPEVALTTDEK Length 542; Indels 0; Gaps 198 78 0;

Search completed: February 25, Job time : 132.743 secs 2005, 02:39:44

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Database
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Listing first 45
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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H9R procein - vari	Schecicar F		accin pre	hypothetical prote	protein-tyrosine k	protein-tyrosine-p	glycoprotein 130 -	cytokine receptor	interleukin-3 rece	interferon recepto	interferon alpha/b	interferon alpha-b	cardia	tissue factor prec	factor	tissue factor prec	tissue factor prec		interferon gamma r	interferon gamma r	interleukin-10 rec		interferon gamma r	interferon alpha/b	interferon alpha r	interferon alpha/b	interferon recepto	cytokine receptor		Description

RESULT 2

hypothetical prote	E86463	N	525	7.2	86.5	5
protein-tyrosine-p	I50213	N	440	7.2	86.5	4
receptor-like tyro	S51605	N	948	7.3	88	43
tyrosine kinase Mp	S49004	N	977	7.4	88.5	ະ
B8R protein - vacc	G42526	N	272	7.4	88.5	Ξ
cytokine receptor	A39255	<u>,</u>	897	7.4	89	ö
leukocyte antigen-	S46216	N	1898	7.5	89.5	9
leukocyte antigen-	TDHULK	_	1897	7.5	89.5	8
frazzled gene prot	T13823	N	1526	7.5	90	7
hypothetic	T19473	N	1526	7.5	90	9
frazzled gene	T13822	N	1375	7.5	90	5
rig-1 protein	T14316	ນ	1344	7.5	90	4.
protein-tyrosine-p	TDFFLK	_	2029	7.6	91.5	ū
B8R 31K protein	JQ1802	N	272	7.6	91.5	Ñ
projectin	T13931	N	6658	7.8	93.5	ï
gene B9R protein	136855	N	266	7.8	93.5	5

ALIGNMENTS

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C;Genetics:
A;Gene: GDB:CRPB4; CRF2-4
A;Crose-references: GDB:138168; OMIM:123889
A;Map position: 21q; 21q22.1-21q22.2
A;Introns: 17/1; 58/2; 111/1; 166/3; 216/1
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A;Title: A new member of the cytokine receptor gene family maps on chromosome A;Reference number: A47003; MUID:93300510; PMID:8314576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Homo sapiens (man)
C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004
C;Accession: A47003; G01418
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A;Residues: 1-123,'D',125-268,'VGRME' <LU2>
A;Cross-references: EMBL:U08988; NID:g571295; PID:g571296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Lutfalla,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-325 <LUT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: A47003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cytokine receptor family class II protein CRF2-4 precursor - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
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A;Reference number: G06935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPROT:Q08334; GB:Z17227; NID:g393378; PIDN:CAA78933.1; PID:g39337
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Matches
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Best Local S
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  182
                                               180 EPNTLYCVHVESFVPGPPRRAQPSEKQCARTLKDQS 215
                                                                                                    131 FLAPKIENEYETW--
                                                                                                                                                 126 LTAP-----EKWKRNPEDLPVSMQQIYSNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWL 179
                                                                                                                                                                                                     74 CDFSSLSKYGDHT--LRVRAEFADEHSDWVNI-TFCPVDDTIIGPPGMQVEVLADSLHMR 130
                                                                                                                                                                                                                                                                                                         19 GMVPPPENVRMNSVNFKNILQWESPAFAKG-NLTFTAQYLSYR----IFQDKCMNTTLTE 73
                                                                                                                                                                                                                                                     66 CDLSAETSDYEHQYYAKVKAIWGTKCSKWAESGRFYPFLETQIGPPEVALTTDEKSISVV 125
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                                                                                                                                                                                                                                                                                                                                    6 GGLPKPANITFLSINMKNVLQWTPDEGLQGVKVTYTVQYFIYGQKKWLNKSECRNINRTY 65
                                                                                                                                                                                                                                                                                                                                                                                                              63;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
EPWTTYCVQVRGFLPDRNKAGEWSEPVCEQTTHDET
                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        19.4%; Score 232.5; DB 2; 29.2%; Pred. No. 3.9e-12; tive 36; Mismatches 94;
                                                                                                    TMKNVYNSWTYNVQYWKNGTDEKFQITPQYDFEVLRNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 325;
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 243-264 <RE3>
A;Cross-references: EMBL:U06239; NID:g497106; PIDN:AAA65004.1;
A;Accession: 148426
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 118-125 < RES>
                                                                                                                                                                                                                                                                                                                                                                                     Gene 148, 343-346, 1994
A;Title: Structure of the murine interferon alpha/beta receptor-encoding gene: high-free A;Reference number: I48423; MUID:95047447; PMID:7958966
A;Accession: I48423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 3
A45283
                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:U06237; NID:g497103; PIDN:AAA65003.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Lutfalla,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 interferon alpha/beta receptor - mouse (;Species: Mus musculus (house mouse) C;Becies: Mus musculus (house mouse) C;Date: 25-Mar-1993 #sequence revuse) C;Date: 25-Mar-1993 #sequence revision 18-Nov-1994 #text_change 09-Jul-2004 C;Accession: A45283; I48423; \overline{I48425}; I48425; I48426; I48427; I48428; I48429 R;Uze, G.; Lutfalla, G.; Bandu, M.T.; Proudhon, D.; Mogensen, K.E. Proc. Natl. Acad. Sci. U.S.A. 89, 4774-4778, 192; Mogensen, K.E. A;Title: Behavior of a cloned murine interferon alpha/beta receptor expresse A;Reference number: A45283; MUID:92262522; PMID:1533935
                                                                                                                                                                                                                                                                      A;Accession: I48424
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interferon
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A;Accession: JC6311
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A; Residues: 1-349 < GIB>
                                                                                                                                                         ;Molecule type: DNA
;Residues: 127-224 <RE2>
;Cross-references: EMBL:U06238; NID:9497104; PIDN:AAC01749.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;Cross-references: UNIPROT:P33896; GB:M89641; NID:g194111; NOte: sequence extracted from NCBI backbone (NCBIN:102354,
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Best Local S
Matches 67
                                                                                                                                                                                                                                      Status: preliminary; translated
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    preliminary; translated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G.; Uze,
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67; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PPEMQIESLAESLELRFSAPQ-IENEPETW--TLKNIYDSWAYRVQYWKNGTNEKFQVVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----FQDHCKRTASTQCDFS-HLSKY-GDYTVRVRAELADEHSEWV-NVTFCPVEDTIIG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KKWLNKSECRNINRTYCDLSAETSDYEHQYYAKVKAIWGTKCSKWAESGREYPFLETQIG 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCVSGGL-----PKPANITELSINMKNVLQWTPPEGLQGVKVTYTVQYFIYGQ 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCVAGWLGGFLLVPALGMIPPPEKVRMNSVNFKNILQWEVP-AFPKTNLTFTAQYESYRS
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Pred. No. 6.3e
35; Mismatches
from GB/EMBL/DDBJ
                                                                                                                                                                                                                                      from GB/EMBL/DDBJ
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                                          PID:g510261
                                                                                                                                                           PID:g755811
                                                                                                                                                                                                                                                                                PID:g755810
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A; Residues: 1-421.'V', 423-560 <LIM>
A; Residues: 1-421.'V', 423-560 <LIM>
A; Cross-references: EMBL:L06320; NID:g163187; PIDN:AAA02571.1; PID:g163188
A; Experimental source: lung
C; Keywords: antiviral; cytokine receptor; transmembrane protein
E;1-24/Domain: signal sequence #status predicted <SIG>
F;25-560/Product: interferon alpha receptor type 1 #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              interferon alpha receptor type 1 precursor - bovine ()Species: Bos primigenius taurus (cattle) (C;Date: 13-Jan-1995 #sequence revision 13-Jan-1995 #text C;Accession: $27387; $33770 R;Mouchel-Vielh, E.; Lutfalla, G.; Mogensen, K.E.; Uze, FBSS Lett. 313, 255-259, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: Specific antiviral activities of the human alpha A;Reference number: S27387; MUID:93076908; PMID:1446745 A;Accession: S27387
                                                                                                                                                    A; Molecule type: mRNA
                                                                                                                                                                          A; Status: preliminary; nucleic acid
                                                                                                                                                                                                    A; Accession: S33770
                                                                                                                                                                                                                     Biochim. Biophys. Acta 1173, 314-319, 1993
A;Title: Cloning and characterization of a
A;Reference number: S33770; MUID:93305725;
                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPROT:Q04790; EMBL:X68443; NID:g431; A;Experimental source: MDBK cells R;Lim, J.K.; Langer, J.A.
                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; nucleic acid sequence not A;Molecule type: mRNA
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A; Residues: 473-590
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A;Residues: 426-445 <RE6>
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A; Residues: 397-424
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A; Residues: 265-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RNINRTYCDLŞAETSDYEHQYYAKVKAIWGTKCSKWAESGRFYPFLETQIGPPEVALTTD 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KIPELLPETTYCLEVKAIHPSLKKHSNYSTVQCIST 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VLTWLEPNTLYCVHVESFVPGPPRRAQPSEKQCART
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QHTTTTKCEFSLLDTNVYIKTQFRVRAEEGNSTSSWNEVDPFIPFYTAHMSPPEVRLEAE 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LPSAAGGENLKPPENIDVYIIDDNYTLKWSSHGESMG-SVTFSAEYRTKDEAKWLKVPEC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL: U06241; NID: 9497110; PIDN: AAA65006.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <RE7>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL: U06240; NID: 9497108; PIDN: AAA65005.1; PID: 9510262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16.3%;
25.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 196; DB 2;
Pred. No. 9.7e-09
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                                                                                                                                                                          sequence not shown
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PMID:8318540
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A;Gene: GDB:IFNAR1; IFNAR; IFRC
A;Cross-references: GDB:120078; OMIM:107450
A;Cross-references: GDB:120078; A;Map position: 21q22.1-21q22.1
A;Introns: 26/1; 67/2; 126/1; 177/3; 225/1; 263/2; 342/1; 381/3; 432/1; A;Introns: 26/1; 67/2; 126/1; 177/3; 225/1; 263/2; 342/1; 381/3; 432/1; C;Keywords: cytokine receptor; glycoprotein; transmembrane protein F;1-21/Domain: transmembrane #status predicted <TRN1>F;437-455/Domain: transmembrane #status predicted <TRN2>F;437-455/Domain: transmembrane #status predicted <TRN2>F;50,58,81,88,110,172,254,313,314,376,416,433,507,518,537/Binding site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ributfalla, G.
Ributfalla, G.
Bubmitted to the EMBL Data Library, July 1991
A:Description: The Structuree of the human in
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A;Title: Genetic transfer of a functional human interferon
A;Reference number: A32694; MUID:90124632; PMID:2153461
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                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;Molecule type: DNA
;Residues: 1-16,'A',18-329,'V',343-557 <LUT>
;Cross-references: EMBL;X60459; NID:g32671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;Molecule type: mRNA;Residues: 1-557 <UZE>;Cross-references: UNIPROT:P17181; GB:J03171; NID:g184645;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Species: Homo sapiens (man)
Date: 22-Jun-1990 #sequence_revision
Accession: A32694; S17112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Reference number: S17112
Accession: S17112
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Best Local
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   192
                                         179
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                                                                                                                                                                                                                                                                                                             51;
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                                                                                                                                                                                                                                                                                                         h 14.0%; Score 168.5; DB 2;
Similarity 26.4%; Pred. No. 1.9e-06;
51; Conservative 35; Mismatches 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                             VIHISPGTK------DSVMWALDGLSPTYSLLIWKNSSGVEERIENIYSRHKIYK--
                                                                                                                                                                                   RTYCDLSAETSDYEHQYYAKVKAIWGTKCSKWAESGRFYPFLETQIGPPEVALTTDEKSI
                                                                                                                 SVVLTAPEKWKRNPEDLPVSMQQIYSNLKYNVSVLNTKSNRTWSQCVTN----HTLVLTW
                                                                                                                                                       STKCNFSSLKLNVYEEIKLRIRA-EKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAI
                                                                                                                                                                                                                                 AGGKNLKSPQKVEVDIIDDNFILRWNRSDESVG-NVTFSFDYQKTGMDNWIKLSGCQNIT
                                       LEPNTLYCVHVES 191
                                                                                                                                                                                                                                                                       SGG--LPKPANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYFIYGQKKWLNKSECRNIN
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   LSPETTYCLKVKA
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28.7%;
   204
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Pred. No. 5.7e-08;
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                                                                                                                                                                                                                                                                                                                                              Length 557;
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A49667
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R;Aguet, M.; Dembic, Z.; Merrin, C.
Cell 55, 273-280, 1988
Cell 55, 273-280, 1988
A;Title: Molecular cloning and expression of the A;Title: Molecular A31555; MUID:89003065; PMID:2
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C; Superfamily: interferon gamma receptor
C; Keywords: cytokine receptor; transmemb
                                                                                                                                                                                         C; Superfamily: interl
C; Keywords: cytokine
                                                                                                                                                                                                           A;Gene: Illor
C;Superfamily: interleukin-10 receptor ILloR
                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-575 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  interleukin-10 receptor - mouse C; Species: Mus musculus (house mouse)
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C;Species: Homo sapiens (man)
C;Date: 28-Feb-1990 #sequence revision
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A31555
                                                                                                                                                                                                                                                     C;Genetics:
                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:Q61727;
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                                                                                                                                                                                                                                                                                                                          Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                   Matches
                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                              Accession:
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Best Local (
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                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                              A49667
LSAETSDYEHQ---YYAKVKAIWGTKCSKWAESGRFYPFLETQIGPPEVALTTDEKSISV 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BIQC----QLAIPVSSLNSQYCVSAE
                                                                                                                 Conservative
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                                                                                                                                                                                           receptor
                                                                                                                                 13.2%;
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                                                                                                             33;
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                                                                                                                                                                                                                                                                       GB:L12120;
                                                                                                                 Mismatches
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R;HO, A.S.; Liu, Y.; Khan, T.A.; Hsu, D.H.; Bazan, J.F.; Moore, Proc. Natl. Acad: Sci. U.S.A. 90, 1127-11271, 1993
A;Title: A receptor for interleukin 10 is related to interferon A;Reference number: A49667; MUID:94068585; PMID:8248239
A;Accession: A49667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:P15260; GB:J03143; NID:g184650; PIDN:AAA52731.1; PID:g30691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 LPKPANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYFIYGQKKWLNKSECRNINRTYCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 LPKPANITFLSINMKNVLQW------TPPEGLQGVKVTYTVQYFIYGQK--KWLNKSEC 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EKSISVVLTAPEKWKRNPED-----LPVSMQQIY----SNLKYNVSVLNTKSNRT 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INISHHYCNISDHVGDPSNSLWVRVKARVGQKESAYAKSEEFAVCRDGKIGPPKLDIRKE 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RNINRTYCDLSAETSDYEHQYYAKVKAIWGTKCSKWAESGRFYPFLETQIGPPEVALTTD 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VPTPTNVTIESYNMNPIVYWEYQIMPQVP-----VFTVEVKNYGVKNSEWID--AC
LPSPSYVWFEARFFQHILHWKPIPN-QSESTYYEVALKQYGNSTWNDIHICRKAQALSCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EKQIMIDIFHPSVFVNGDEQEVDYDPETTCYIRVYNVYVRMNGSEIQYKI-LTQKEDDCD 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transmembrane protein
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Pred. No. 4.2e-06;
                                                                                                                               Score 159; DB 2;
Pred. No. 1.2e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-Feb-1990
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                                                                                                                                                                                                                                                                                                                       NID:g437615; PIDN:AAA16156.1; PID:g43761.
                                                                                                         100;
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                                                                                                                                                      Length 575
                                                                                                         Indels
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                                                                                                         32;
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                                                                                                      Gaps
  84
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interferon gamma receptor beta subunit - mouse
N;Alternate names: IFN-gamma R beta chain; IFN-gamma R species-specific cofactor;
C;Species: Mus musculus (house mouse)
C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A49947
   A; Note: sequence
                                                                                                                                                                                                                                                                                                          RESULT 9
A49947
           A;Cross-references: UNIPROT:Q63953; GB:S69336; NID:g545841; PIDN:AAB30165.1; PID:g545842
A;Experimental source: early B-cell line Y16
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                                                       A; Residues: 1-332 < HEM>
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A;Map position: 11q23.3-11q23.3
C;Superfamily: interleukin-10 receptor IL10R
C;Keywords: Cytokine receptor
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A; Residues: 1-578 < RES>
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A;Title: Expression cloning and characterization of a human IL-10

A;Reference number: I56215; MUID:94165477; PMID:8120391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; Liu, Y.; Wei, S.H.; Ho, A.S.; de Waal Malefyt, R.; Moore,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: GDB: IL10R; HIL-10R
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C;Species: Homo sapiens (man)
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                                                                             Molecule type: mRNA
                                                                                             Status: preliminary
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           136 NGFILGKIQLPRPKMAPAND-----TYESIFSHFREYEIAIRKVPGNFTFTHKKVKHENF
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                                                                                                                                                                                                                                                                                                                                                                                    SLLTSGEVGE-FCVQVKPSVASRSNKGMWSKEEC
                                                                                                                                                                                                                                                                                                                                                                                                                      LVLTWLEPHTLYCVHVESFVPGPPRRAQPSEKQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LTAVTLDLYHSNGYRARVRAVDGSRHSNWTVT-----NTRFSVDEVTLTVGSVNLEIH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HTLVLTWLEPNTLYCVHVESFVPGPPRRAQPSEKQCARTLKDQ 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----SVVLTAPEKWKRNPEDLPVSMQQIYSNLK-YNVSVLNTKSNRTWSQCVTNHT-- 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TLKAMDGIIYGTIHPPR----PTITPAGDEYEQVFKDLRVYKISIRKFSELKNATKRVKQ 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VLTA-----PEKWKRNPEDLPV--SMQQIYSNLK-YNVSVLNTKSNRTWSQCVTN 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ETFTLTVPIGVRKFCVKVLPRLESRINKAEWSEEQCLLITTEQ 232
   extracted from NCBI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.9%;
24.8%;
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Pred. No. 0.00028;
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   backbone
(NCBIN:145654,
                                                                                                                                                                                                                                                                                                                                                                                    223
                                                                                                                                                                                                                                                                                                                                                                                                                        207
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A; Molecule type: mRNA
A; Residues: 1-94, 'E', 96-477 <HEM>
A; Residues: 1-94, 'E', 96-477 <HEM>
A; Cross-references: GB: MZ8233; NID: g194131; PIDN: A; Munro, S; Maniatis, T.
R; Munro, S; Maniatis, T.
Broc. Natl. Acad. Sci. U.S.A. 86, 9248-9252, 1989
Proc. Natl. Acad. Sci. U.S.A. 86, 9248-9252, 1989
                                                                                                                                                                                                                                                                                                                                                               A;Molecule Type: mRNA
A;Residues: 1-94, E; 96-477 <GRA>
A;Residues: 1-94, E; 96-477 <GRA>
A;Cross-references: GB.M26711; NID:g194126; PIDN:AAA37896.1;
A;Cross-references: GB.M26711; NID:g194126; PIDN:AAA37896.1;
R;Hemmi, S.; Peghini, P.; Metzler, M.; Merlin, G.; Dembic, Z.
Proc. Natl. Acad. Sci. U.S.A. 86, 9901-9905, 1989
A;Title: Cloning of murine interferon gamma receptor cDNA: ex
A;Reference number: A34508; MUID:90099370; PMID:2532365
A;Accession: A34508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  interferon gamma receptor precursor - mouse C;Species: Mus musculus (house mouse)
C;Date: 08-Jun-1990 #sequence revision 08-Jun-1990 #text change 09-Jul-2004
C;Accession: A34368; A35468; Ā34423; A34508; A36224; I48941
R;Kumar, C.S.; Muthukumaran, G.; Frost, L.J.; Noe, M.; Ahn, Y.H.; Mariano, J. Biol. Chem. 264, 17939-17946, 1989
A;Title: Molecular characterization of the murine interferon gamma receptor A;Reference number: A34368; MUID:90036866; PMID:2530216
A; Molecule type: mRNA
A; Residues: 10-477 < M
                                                          A; Status: preliminary
                                                                                   A; Title: Expression cloning of the murine interferon gamma A; Reference number: A36224; MUID:90083245; PMID:2531896 A; Accession: A36224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:J05265; NID:g197964; PIDN:AAA39178.1; PID:g309394
R;Gray, P.W.; Leong, S.; Fennie, B.H.; Farrar, M.A.; Pingel, J.T.; Fernandez-Luna, J.
Proc. Natl. Acad. Sci. U.S.A. 86, 8497-8501, 1989
A;Title: Cloning and expression of the cDNA for the murine interferon gamma receptor.
A;Reference number: A34423; MUID:90046824; PMID:2530582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Biol. Chem. 265, 4064-4071, 1990
A;Title: Affinity purification, peptide analysis, and cDNA sequence of the mouse interf-
A;Reference number: A35468; MUID:90154099; PMID:2137461
A;Accession: A35468
                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
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A; Residues: 1-477 < COF>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: A34368; A; Accession: A34368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WLEPNTLYCVHVESFVPGPPRRAQP----SEKQCARTLKDQSSEFK 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLVIHFSP----PFD-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LAAPLNPRLHLYNDEQILTWEPSPSSNDPRPVVYQVEYSFIDGSWHRLLEPNCTDITETK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                           PIDN:AAA37898.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                 receptor cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                               expression in
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S.; Appella, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PID:g309330
                                                                                                                                                                                                                                              PID:g309331
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Pestka

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C;Species: Homo sapiens (man)
C;Date: 16-Feb-1996 #sequence revision 16-Feb-1996 #text_change 09-Jul-2004
C;Accession: I38500; I38501
R;Soh, J; Donnelly, R.J.; Kotenko, S.; Mariano, T.M.; Cook, J.R.; Wang, N.; Emanuel Cell 76, 793-802, 1994
A;Title: Identification and sequence of an accessory factor required for activation A;Reference number: A49946; MUID:94170380; PMID:8124716
A;Accession: I38500
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A;Residues: 1-63,'Q',65-337 <RE2>
A;Cross-references: EMBL:U05877; NID:g463551; PIDN:AAA16956.1; PID:g463552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-337 <RES>
A;Cross-references: UNIPROT:P38484;
A;Experimental source: clone pSK1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:M28995; NID:g194123; PIDN:AAA37895.1; PID:g309329 R;RAVA1, P.; Obici, S.; Russell, S.W.; Murphy, W.J. Gene 154, 219-223, 1995 Gene 154, 219-223, 1995 Gene 154. Pip:Marking region and gene encoding the A;Title: Characterization of the 5' flanking region and gene encoding the A;Reference number: I48941; MUID:95197006; PMID:7890167 A;Accession: I48941
A;Status: translation not shown; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
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Best Local S
Matches 55
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Best Local
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    149
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                                                                                                                                                                                                                                                                                                                                                                        cytokine receptor
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                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                     LPAPOHPKIRLYNAEQVLSWEPVALSNSTRPVVYRVQ-FKYTDSKWFTADIMSIGVNCTQ 88
                                                                                                                                                                                                                                LPKPANITFLSINMKNVLOWTPPEGLQGVK-VTYTVQYFIYGQKKWLNKS-----ECRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C--NETLCELNISVSTLDSRYCISVDGISSFWQVRTEKSKDVCIPPFHDDRKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LVFHPE-----VVVNGESQGTMFGDGSTCYTFDYTVYVEHNRSGEILHTKHTVEKEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VPVPTNVLIKSYNLNPVVCWE----YQNMSQTPIFTVQVKVY-SGSWTD--SCTNISDHC
                                             ITATECDETÄASESAGEEMDENVTLRLRÄBLGALHSAWVTMEWEQHYRNVTVGEENIEV 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CVTNHTLVLTWLEPNTL---YCVHVESFVPGPPRRAQPSEKQCARTLKDQSSE 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VLTAPEKWKRNPEDLPVSMQQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CNIYGQIMYPDVSAWARVKAKVGQKESDYARSKEFLMCLKGKVGPPGLEIRRKKEEQLSV
TPGEGSLIIRFSSPFDIADTSTAFFCYYVHYWEKG-----GIQQVKGPFRSNSISLDNL
                                                                                                                                       INRTYCDLSAETSD----YEHQYYAKVKAIWGTKCSKWAESGRFYPFLETQIGPPE-VAL 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDLSAETSDYEHQYYAKVKAIWGTKCSKWAESGRFYPFLETQIGPPEVAL-TTDEKSISV
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                                                                                                                                                                                                                                                                                                  11.4%; Score 136.5; DB 2
22.5%; Pred. No. 0.00051;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            accessory factor-1 precursor - human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL: U05875; NID: g463549; PIDN: AAA16955.1; PID: g463
                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                              102;
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A;Map position: 1922-1921
A;Introns: 34/1; 71/2; 138/1; 197/3; 251/1
A;Introns: 34/1; 71/2; 138/1; 197/3; 251/1
C;Superfamily: tissue factor
C;Keywords: blood coagulation; glycoprotein; lipoprotein; thiolester
C;Keywords: blood coagulation; glycoprotein; lipoprotein; thiolester
F;1-32/Domain: signal sequence #status predicted <SIC>
F;33-251/Pomain: extracellular #status predicted <EXT>
F;33-251/Pomain: extracellular #status predicted <EXT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: mRNA
A;Residues: 1-259, 'A', 261-295 <SCA>
A;Crose-references: GB:M16553; NID:g339503; PIDN:AAA61151.1; PID:g339504
A;Bach, R.; Konigsberg, W.H.; Nemerson, Y.
Biochemistry 27, 4227-4231, 1988
A;Title: Human tissue factor contains thioester-linked palmitate and ste
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A;Title: Molecular cloning of the cDNA for tissue factor, A;Reference number: A29062; MUID:87244317; PMID:3297348
A;Accession: A29062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Reference number: A37422; MUID:89000604; PMID:3166978 A;Roftents: annotation; disulfide bonds and fatty acid binding site C;Comment: Tissue factor is an integral membrane: glycoprotein that (C;Comment: Expression of tissue factor can be induced in a variety (C;Comment: Expression of tissue factor can be induced in a variety (C;Comment: Expression of tissue factor can be induced in a variety (C;Comment: Expression of tissue factor can be induced in a variety (C;Comment: Expression of tissue factor can be induced in a variety (C;Comment: Expression of tissue factor can be induced in a variety (C;Comment: Expression of tissue factor can be induced in a variety (C;Comment: Expression of tissue factor can be induced in a variety (C;Comment: Expression of tissue factor can be induced in a variety (C;Comment: Expression of tissue factor can be induced in a variety (C;Comment: Expression of tissue factor can be induced in a variety (C;Comment: Expression of tissue factor can be induced in a variety (C;Comment: Expression of tissue factor can be induced in a variety (C;Comment: Expression of tissue factor can be induced in a variety (C;Comment: Expression of tissue factor can be induced in a variety (C;Comment: Expression of tissue factor can be induced in a variety (C;Comment: Expression of tissue factor can be induced in a variety (C;Comment: Expression of tissue factor can be induced in a variety (C;Comment: Expression of tissue factor can be induced in a variety (C;Comment: Expression of tissue factor can be induced in a variety (C;Comment: Expression of tissue factor can be induced in a variety (C;Comment: Expression of tissue factor can be induced in a variety (C;Comment: Expression of tissue factor can be induced in a variety (C;Comment: Expression of tissue factor can be induced in a variety (C;Comment: Expression of tissue factor can be induced in a variety (C;Comment: Expression of tissue factor can be induced in a variety (C;Comment: Expression of tissue factor can be induced in a variety (C;Comment: Expres
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Spicer, B.K.; Horton, R.; Bloem, L.; Bach, R.; Williams, Proc. Natl. Acad. Sci. U.S.A. 84, 5184-5152, 1987
A;Title: Isolation of cDNA clones coding for human tissue A;Reference number: A94171; MUID:87260946; PMID:3037536
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Thromb. Res. 48, 89-99, 1987
A;Title: Cloning and expression of human tissue factor cDNA.
A;Reference number: A47574; MUID:88100453; PMID:3424286
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C;Date: 30-Sep-1993 #sequens revision 30-Sep-1993 #text change c;Date: 30-Sep-1993 #sequens C;Accession: A43645; A47574; A28320; A29062; A29672; A29008
R;Maccession: A43645; A47574; A28320; A29062; A29672; A29008
R;Mackman, N.; Morrissey, J.H.; Fowler, B.; Edgington, T.S.
Biochemistry 28, 1755-1762, 1999
B;Title: Complete sequence of the human tissue factor gene, A hi. A;Reference number: A43645; MUID:89247359; PMID:2719931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: GDB:F3
A;Cross-references: GDB:119895; OMIM:134390
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A; Residues: 1-295 < MOR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Genetics:
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A; Residues: 1-295 <SPI>
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A; Residues: 1-295 < FIS>
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252-274/Domain: transmembrane #status predicted 275-295/Domain: intracellular #status predicted
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Flandermeyer, R.R
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A;Title: Cloning of murine tissue factor and regulation of gene expression by transformi A;Feference number: A39046; MUID:91093171; PMID:1985911
A;Accession: A39046
A;Molecule type: mRNA
A;Residues: 1-25,'I',27-294 <RAN>
A;Cross-references: GB:M57896; GB:J05713; NID:g201926; PIDN:AAA63400.1; PID:g201927
A;Cross-references: GB:M57896; GB:J05713; NID:g201926; PIDN:AAA63400.1; PID:g201927
A;Ote: 26-Thr was also found
C;Comment: Tissue factor is an integral membrane glycoprotein that serves as a receptor C;Comment: Expression of tissue factor can be induced in a variety of tissues by certain C;Superfamily: tissue factor
C;Keywords: blood coagulation; glycoprotein; lipoprotein; thiolester bond; transmembrane F;1-29/Domain: signal sequence #status predicted <SIG-FT: 10-294/Domain: signal signal signal sequence #status predicted <SIG-FT: 10-294/Domain: signal signal signal signal status signal status signal signal signal signal status signal si
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A;Title: A growth factor-responsive gene of murine BALB/c 3T3
A;Reference number: A32318; MUID:89343974; PMID:2761539
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                                                                                  CDLSAE-TSDYEHQYYAKVKA-----
                                                                                                                                                  GIPEKAFNLTWISTDFKTILEWOP----KPTNYTYTVO-ISDRSRNWKNK--CFSTTDTE
                                                                                                                                                                                                                          GLPKPA-NITFLSINMKNVLQWTPPEGLQGVKVTYTVQYFIYGQKKWLNKSECRNINRTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VNVTVEDERTLVRRNNTFL--SLRDVFGKDLIYTLYYWKSSSSGK-KTAKTNTNEFLIDV 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VVLTAPEK----WKRNPEDLPVSMQQIY-SNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VKDVKQTYLARVFSYPAGNVESTGSAGEPLYENSPEFTPYLETNLGQPTIQ-SFEQVGTK 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TSDYEHQYYAKVKAIWGTKCSKWAESG-----RFYPFLETQIGPPEVALTTDEKSIS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NLTWKSTNFKTILEWEP----KPVNQVYTVQ---ISTKSGDWKSKCFYTTDTECDLTDEI
           CDLTDEIVKDVTWAYEAKVLSVPRRNSVHGDGDQLVIHGEE-PPFTNAPKFLPYRDTNLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DKGENYCFSVQAVIPSRTVNRKSTDSPVEC---MGQEKGEFR
                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                       11.0%;
25.1%;
                                                                                                                                                                                                                                                                                                  ; Score 131.5; DB
; Pred. No. 0.0011;
38; Mismatches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 135.5;
Pred. No. 0.0
                                                                                  ----IWGTKCSKWAESGRFYPFLETQIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.00053;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                                                     76;
                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
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                                                                                                                                                                                                                                                                                                                                                                         294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      295;
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                                                                                                                                                                                                                                                                                                     47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     predicted
                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                  109
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       N;Alternate
hissue factor precursor - bovir N;Alternate names: coagulation
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 33-292 < PMB>
A; Residues: 33-292 < PMB>
A; Cross-references: EMBL: X53521; NID: g1495; PIDN: CAA37597.1; PID: g3980170
A; Cross-references: EMBL: X53521; NID: g1495; PIDN: CAA37597.1; PID: g3980170
A; Cross-references: EMBL: X53521; NID: g1495; PIDN: CAA37597.1; PID: g3980170
C; Comment: Expression of tissue factor can be induced in a variety of tissues by certain C; Comment: Expression of tissue factor
C; Keywords: blood coagulation; glycoprotein; lipoprotein; thiolester bond; transmembrand C; Lipoprotein: signal sequence #status predicted <SIG>
E; 1-32/Domain: signal sequence #status predicted <AMT>
E: 0.20 no. // Darading: tissue factor #status predicted <AMT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;41,114,154,167,182/Binding site: carbohydrate (Asn) (covalent) F;79-87,216-239/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;250-271/Domain: transmembrane #status predicted <TMM>F;272-292/Domain: intracellular #status predicted <INT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;33-249/Domain: extracellular #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Pawashe, A.; Ezekowitz, M.; Lin, T.C.; Horton, R.; Bach, R.; Konigsberg, W. Thromb. Haemost. 66, 315-320, 1991
A;Title: Molecular cloning, characterization and expression of cDNA for rabbit brain A;Reference number: S23681; MUID:92081032; PMID:1746002
A;Accession: S23681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N,Alternate names: coagulation factor III
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993
C;Accession: JU0441; S23681
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Title: Conservation of tissue factor primary sequence A; Reference number: JU0441; MUID:91200676; PMID:1840552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gene 98,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ś
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Experimental source: brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R; Andrews, B.S.; Rehemtulla, A.; Fowler, B.J.; Edgington,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Residues: 1-292 < AND>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tissue factor precursor - rabbit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;274/Binding site: palmitate (Cys)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cross-references: UNIPROT:P24055; GB:M55390; NID:g165696; PIDN:AAA63469.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14
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        198
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                                                                                                                                                                                                                                      94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51;
ATTNTNEFLIDVDKGENYCFSVQAVIPSRKKKQRSPESLTECTSREQ
                                                           CVTNHTLVLTWLEPNTLYCVHVESFVPGPPRRAQPSEKQCARTLKDQ 214
                                                                                                                 -----QSFEQVGTKLNVTVQDARTLVRRNGTFLSLRAVFGKDLNYTLYYWRASSTGKKT 197
                                                                                                                                                                       VVLTAPEKWKRNPEDLPVSMQQIYSNLKYNVSVLNTKS-----NRT---W-----SQ 167
                                                                                                                                                                                                                                                                                            TSDYEHQYYAKVKAIWGTKCS-----KWAESGRFYPFLETQIGPPEVALTTDEKSIS 123
                                                                                                                                                                                                                                                                                                                                                  NLTWKSTNFKTILEWEP----KSIDHVYTVQ-ISTRLENW--KSKCFLTAETECDLTDEV
                                                                                                                                                                                                                                                                                                                                                                                                           NITFLSINMKNVLQWTPPEGLQGVKVTYTVQYFIYGQKKWLNKSECRNINRTYCDLSAE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFV 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PPEV-ALTTDEKSISVV----LTAPEKWKRNPEDLPVSMQQIY-SNLKYNV-----SVLN
                                                                                                                                                                                                                                      VKDVGQTYMARVLSYPARNGNTTGFPEEPPFRNSPEFTPYLDTNLGQPTI--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KKTN-----ITNTNEFSIDVEEGVSYCFFVQAMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 130; DB 1; Length 292; Pred. No. 0.0015; 9; Mismatches 89; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #text_change 09-Jul-2004
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     244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #status
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A,Experimental source: adrenal gland
A,Note: part of this sequence, including the amino end of the mature protein, was confix
C,Comment: Tissue factor is an integral membrane glycoprotein that serves as a receptor
C,Comment: Expression of tissue factor can be induced in a variety of tissues by certain
C,Superfamily: tissue factor
C,Keywords: blood coagulation; glycoprotein; lipoprotein; thiolester bond; transmembrane
F,135/Domain: signal sequence #status predicted <SIG-
F,135/Domain: extracellular #status predicted <EXT-
F,246-271/Domain: transmembrane #status predicted <INT-
F,272-292/Domain: intracellular #status predicted <INT-
F,43,153,181/Binding site: carbohydrate (Abn) (covalent) #status predicted
F,118,124/Binding site: palmitate (Cys) (covalent) #status predicted
F,274/Binding site: palmitate (Cys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: JQ1319
R;Takayenoki, Y:; Muta, T:; Miyata, T:; Iwanaga, S.
Blochem. Biophys. Res. Commun. 181, 1145-1150, 1991
A;Title: cDNA and amino acid sequences of bovine tissue factor.
A;Reference number: JQ1319; MUID:92109720; PMID:1764065
A;Accession: JQ1319
Search completed: February 25, 2005, 02:45:37 Job time : 27.5401 secs
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A;Molecule type: mRNA
A;Residues: 1-292 <TAK>
                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 53; Conserv
                                                                                                                                     200 NTNGFLIDVDKGENYCFHVQAVILSRRVNQKSPESPIKCTSHEK 243
                                                                                                                                                                                                    171
                                                                                                                                                                                                                                                                143 --- QSFEQVGTKLNVTVQDARTLVRANSAFLSLRDVFGKDLNYTLYYMKASSTGKKKATT
                                                                                                                                                                                                                                                                                                                                      127 TAPEKWKRNPEDLPVSMQQIYSNLKYNVSVLNTKS-----NRT---W------SQCVT 170
                                                                                                                                                                                                                                                                                                                                                                                                         96 VKNVRETYLARVLSYPADTSSSTVEPPFTNSPEFTPYLETNLGQPTI------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72 TSDYEHQYYAKVKAIWGTKCSKWAE----SGRFYPFLETQIGPPEVALTTDEKSISVVL 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 NITFLSINMKNVLOWTPPEGLOGVKVTYTVQYFIYGQKKWLNKSECRNINRTYCDLSAE-
                                                                                                                                                                                                    NHTLVLTWLEPNTLYCVHVESFV-----PGPPRRAQPSEK 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NITWKSTNFKTILEWEP----KPINHVYTVQ-ISPRLGNWKNK--CFYTTNTECDVTDEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10.8%; Score 129; DB 1; Length 292; 23.7%; Pred. No. 0.0018; tive 32; Mismatches 85; Indels
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SUMMARIES

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Abg75853	Abu66861	Abu59388	Abu92323	Abu58945	Abu80391	Abo24856	Abo25936	Abu59239	Abu61122	Abu59666	Abu84924	Abu66585	Abu72490	Abu72244	Abu80885	Abu13905	Abo25238	Abu60523	Abo17631
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ALIGNMENTS

28-JUN-2001. WO200146232-A2 Homo sapiens. dermatological; Interleukin 20; IL-20; IL-20RA; ZcytoR7; IL-20RB; DIRS1; immunoglobulin; antiinflammatory; antipsoriatic; antiasthmatic; antibacterial; human; 07-SEP-2001 Human IL-20 receptor subunit IL-20RB extracellular domain fragment. AAB85271; AAB85271 standard; protein; (first entry) antiulcer; antagonist. 203 ₽

23-DEC-1999; 99US-00471774. 22-JUN-2000; 2000US-0213416P.

22-DEC-2000; 2000WO-US035307

(ZYMO) ZYMOGENETICS INC.

Foster DC, Xu W, Madden Rixon MW, Presnell SR, F

n KL, Ka Fox BA;

Kelly JD,

Sprecher CA,

Brandt CS;

Isolated interleukin 20 soluble receptor comprising two polypeptide subunits IL-20RA and IL-20RB, useful for down-regulating IL-20 and thus treating inflammatory diseases such as psoriasis. WPI; 2001-398320/42.

Claim 1; Page 69; 119pp; English.

The invention relates to an interleukin 20 (II-20) soluble receptor comprising two polypeptide subunits II-20RA (formerly known as ZcytoR7) and II-20RB (formerly known as IRS1). The two subunits are preferably linked together. In one embodiment, one subunit is fused to the constant region of the light chain of an immunoglobulin, and the other subunit is fused to constant region of the heavy chain of an immunoglobulin. The light chain and the heavy chain are connected via a disulphide bond. The soluble receptor can be used to down-regulate II-20 and thus treat inflammatory diseases such as psoriasis, inflammatory lung injury such as asthma or bronchitis, adult respiratory disease (ARD), septic shock,

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Matches 203
                                                                                                                                                                                                                                                                                                      Inflammation; interleukin-20; IL-20; interleukin-8; IL-8; chemokine; neutrophil; monocyte; basophil; eosinophil; chemoattractant; psoriasis; periodontal disease; rheumatoid arthritis; idiopathic pulmonary fibrosis; angiogenesis-dependent chronic inflammatory condition; lung cancer; melanoma; inflammatory disease; diabetes; arteriosclerosis; cataract; reperfusion injury; cancer; meningitis; rheumatic disease; skin disease; idiopathic pulmonary fibrosis; inflammatory bowel disease; psoriasis; inflammatory contact dermatitis; contact dermatitis; inflammatory lung disease; ARD; adult respiratory disease; asthma;
   Thompson
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(JASP/)
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22-JUN-2000;
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                         MADDEN K L.

KELLY J D.

SPRECHER C A.

SERECHER C A.

BLUMBERG H.

BAGAN M A.

JASPERS S R.

CHANDRASEKHER Y P.

NOVAK J E.
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Sequence

203

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CC The invention describes a method (I) for treating a mammal afflicted with CC a disease in which an interleukin-20 (IL-20) polypeptide plays a role CC comprising administering antagonist of the IL-20 polypeptide to the CC comprising administering antagonist of the IL-20 polypeptide to the CC individual. An important cytokine in the inflammatory process is CC interleukin-8 (IL-8), a chemokine that acts as an agonist for neutrophils controlled to the release of granule enzymes. IL-8 binds to controlled the release of granule enzymes. IL-8 binds to controlled the release of granule enzymes. IL-8 binds to controlled the release of granule enzymes. IL-8 binds to controlled the release of granule enzymes. IL-8 binds to controlled the release of granule enzymes. IL-8 binds to controlled the release of granule enzymes. IL-8 binds to controlled the release of granule enzymes. IL-8 binds to controlled the release of granule enzymes. IL-8 binds to controlled the release of granule enzymes. IL-8 binds to controlled the release of granule enzymes. IL-8 is an controlled the release of angiogenesis in several angiogenesis-dependent controlled the source of angiogenic activity in human lung cancer. Also, IL-8 controlled the controlled the expression correlates with experimental metastatic activity of some controlled the controlled the experimental metastatic activity of some controlled the treat these diseases. The method to treat inflammatory controlled the service of seases including diabetes. The method is used for treating controlled the service of seases including diabetes, arteriosclerosis, cataracts, reperfusion conflictions. The method is used for treating controlled the service of seases (alphabetic pulmonary controlled the service of seases, idiopathic pulmonary controlled the service of seases (alphabetic pulmonary controlled the service of seases (alphabetic pulmonary controlled the service of seases (alphabetic pulmonary controlled the service of seases, idiopathic pulmonary controlled the service of seases (alp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Treating inflammatory skin and lung diseases using antibodies against interleukins (IL)-20 (which indirectly modulates activation of IL-8), useful for treating e.g. psoriasis, asthma and bronchitis.
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ID AAE2
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DE Huma
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UM Huma
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AC Huma
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Human interleukin-20 receptor beta variant (V-IL-20RB) Ö domain.

27-AUG-2002

Human; interleukin-19; IL-19; interleukin-20 receptor beta; diabetes; reperfusion injury; interleukin-20 receptor alpha; IL-20RA; IL-20RB; inflammation; atherosclerosis; cancer; infectious meningitis; cataract

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RESULT 4
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                         Human IL-22RB protein
                                                                                                          AAE29065 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 comprises administration of a polypeptide comprised domain of IL-20RA and IL-20RB.
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Synthetic.
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heterodimeric cytokine receptor;
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                                                                                                                                                                                                                                                                                   SLTEGPECOVTODITATVPYNLRVRATLGSQTSAWSILKHPFNRNSTILTRPGMEITKDG
                                                                                                                                                                                                                                                                                                                                         DEVAILPAPQNLSVLSTNMKHLLMWSPVIAPGETVYYSVEYQGEYESLYTSHIWIPSSWC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Page 51-52; 80pp; English
                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ₹
                                                    (first entry)
                                                                                                          protein;
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Pred. No. 5.1e-109;
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                                                                                                                                                                            203
interleukin-22R;
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IL-22R;
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asthma;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              failure, septic shock, inflammatory lung injury such as bronchitis asthma, bacterial pneumonia, eczema, atopic and contact dermatitis, ulcerative colitis and Crohn's disease. The present sequence is hum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to novel heterodimeric cytokine receptor which comprises an interleukin-22R (IL-22R, ZcytoRil)) subunit. Receptor sequences are useful for down-regulating IL-20 and treating inflammatory diseases such as psoriasis, adult respiratory disease, multiple organ failure, septic shock, inflammatory lung injury such as bronchitis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Soluble heterodimeric cytokine receptor useful for down-regulating interleukin-20 and treating inflammatory diseases, such as psoriasis and asthma, comprises an interleukin-22R subunit and a interleukin-20RB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-MAR-2001; 2001US-0274560P
21-JUN-2001; 2001US-0299865P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inflammatory disease; psoriasis; adult respiratory disease; bronchitis; septic shock; multiple organ failure; inflammatory lung injury; eczema; bacterial pneumonia; dermatitis; ulcerative colitis; Crohn's disease;
                                                                                                               ADJ83295 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 59-60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         subunit.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    interleukin-22RB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (IL-22RB) protein
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                                                                                                              protein;
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Human interleukin receptor IL-20RB

extracellular domain interleukin;

mature protein. IL-20RA subunit;

IL-20;

inflammation; single chain antibody;

06-MAY-2004

(first entry)

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Query Match
Best Local S
Matches 203
                                                                                                                                                                                                                                                                                                                           The invention relates to a novel method of reducing or treating inflammation in a mammal which comprises administering an antibody, antibody fragment or single chain antibody which specifically binds to a receptor of interleukin (II)-20 comprising an IL-20RA subunit and an IL-20RB subunit. The method of the invention has antiinflammatory, dermatological, antipsoriatic, antiarthritic, respiratory, antiasthmatic, applications and may be useful for reducing or treating an inflammatory including an inflammatory skin disease such as psoriasis, eczema, atopic dermatitis and contact dermatitis or an inflammatory lung disease such as adult respiratory distress syndrome, asthma, bronchitis and pneumonia, as well as arthritis, septic shock, multiple organ failure, inflammatory bowel disease, ulcerative colitis or Crohn's disease. The current sequence is that of the human IL-20RB subunit-related protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Reducing or treating inflammation, e.g. inflammatory lung disease, comprises administering an antibody, antibody fragment or single chain antibody that specifically binds to an interleukin (IL)-20RA subunit of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IL-20RB subunit; antiinflammatory; dermatological; antipsoriatic; antiarthritic; respiratory; antiasthmatic; antiulcer; antibacteri immunosuppressive; gastrointestinal; skin; psoriasis; eczema; atopic dermatitis; contact dermatitis; lung; adult respiratory distress syndrome; asthma; bronchitis; pneumoni arthritis; septic shock, multiple organ failure; bowel; ulcerative colitis; Crohn's disease; human; receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    comprises administering an antibody, antibody that specifically binds to an IL-20 receptor.
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Blumberg H,
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22-JUN-2000; 2000US-0213341P.
22-DEC-2000; 2000US-00746359.
                                                                                                                                                                                                                                                         Sequence 203
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(SPRE/)
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203; Conserv
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KELLY J D.

SPRECHER C A.

SPRECHER C A.

BLUMBERG H.

BAGAN M A.

DASPERS S R.

CHANDRASEKHER Y A.

NOVAK J E.
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SLTEGPECDVTDDITATVPYNLRVRATLGSQTSAWSILKHPFNRNSTILTRPGMEITKDG
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                                                                                                                                                    100.0%; Score 1080; DB 8; ilarity 100.0%; Pred. No. 5.1e-109; Conservative 0; Mismatches 0;
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Bagan MA,
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kasekher YA,
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Novak JE;
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13-MAR-1998;
17-MAR-1998;
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20-MAR-1998;
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11-MAR-1998;
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                                                                                                                                                                                                                                                                      20-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY41736 standard;
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98US-0078939P.
98US-0079294P.
98US-0079556P.
98US-0079663P.
98US-0079664P.
98US-0081071P
98US-0081195P
98US-0081229P
98US-0081817P
98US-0081817P
98US-0081838P
98US-0081955P
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98US-0078886P.
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                                                                    3-0081070P.
3-0081071P.
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-0079920P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     hybridisation;
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The present invention describes secreted and transmembrane polypeptides and their polynucleotides. The nucleotide sequences are useful as sources of probes, primers, for chromosome mapping, and for generation of antisense sequences. They can also be used to create transgenic animals. The proteins can be used to treat a variety of diseases and disorders, depending on their function. Diseases that may be treated include blood cosgulation disorders, cancers (callular adhesion disorders. They may also be used to raise antibodies. AAZ33381 to AAZ34338, and AAY41685 to AAY41774 represent polynucleotide and polypeptide sequence given in the exemplification of the present invention
                                                                                                                               Claim
                                                                                                                                                    New secreted and transmembrane polypeptides and useful for treating blood coagulation disorders, adhesion disorders.
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N-PSDB; AAZ34190.
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                                                                                                                             12; Fig 142; 530pp;
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                                                                                                                                    The invention provides membrane-bound PRO polypeptides and polynucleotides encoding them. The PRO sequences of the invention were identified based on extracellular domain homology screening. The PRO sequences have homology with proteins including LDL receptors, TIE ligands and various enzymes. The membrane-bound proteins and receptor molecules are useful as pharmaceutical and diagnostic agents. Receptor immunoadhesins, for instance, can be used as therapeutic agents to block receptor-ligand interactions. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. The PRO encoding sequences are useful as hybridization probes, in chromosome and gene mapping and in the generation of antisense RNA and DNA. PRO nucleic acid sequences will also be useful for the preparation of PRO polypeptides, especially by recombinant techniques
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                                                                                                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes sixty four human PRO proteins which can CC be used in the treatment of immune related diseases. The human PRO proteins, anti-PRO antibodies, agonists and antagonists are useful for CC proteins, anti-PRO antibodies, agonists and antagonists are useful for CC treating and diagnosing immune related disorders. The disorders are selected from systemic lupus erythematosus, rheumatoid arthritis, contected from systemic lupus erythematosus, rheumatoid arthritis, contected from systemic lupus erythematosus, rheumatoid arthritis, contected from systemic vasculitis, sarcoidosis, autoimmune haemolytic content of the control and content of the control of the control and content of the lung, and transplantation associated disease, autoimmune cor immune-mediated skin diseases, allergic diseases, inflammatory bowel content of the lung, and transplantation associated diseases including cor immune-mediated skin diseases, allergic diseases, immunological cor immune-mediated skin diseases, allergic diseases, insmunological cor immune-mediated skin diseases, allergic diseases, allergic diseases including cor immune-mediated skin diseases, allergic dis
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Best Local S
Matches 203
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02-DEC-1999; 99WO-US0308565.
16-DEC-1999; 99WO-US030095.
20-DEC-1999; 99WO-US030999.
30-DEC-1999; 99WO-US031274.
05-JAN-2000; 2000WO-US000277.
06-JAN-2000; 2000WO-US000376.
11-FEB-2000; 2000WO-US0003565.
18-FEB-2000; 2000WO-US004341.
18-FEB-2000; 2000WO-US004341.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sixty four PRO polypeptides, useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosis, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 33; Fig 54; 309pp; English
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N-PSDB; AAC58605.
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Kabakoff RC,
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ff RC, Lu Y, P
t TA, Tumas D,
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KAIGRYSAFSQTECVEVQGEAIP
                       KAIGRYSAFSQTECVEVQGEAIP
                                                                                                                  FHLVIELEDLGPQFEFLVAYWRREPGAEEHVXMVRSGGIPVHLETMEPGAAYCVKAQTFV
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                                                                                                                                                                                                                                                                                                                                                                  Conservative
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100.0%; Pred. No. 9.8e-109;
tive 0; Mismatches 0;
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Pan J, Pennica D; Shelton DL,
, Watanabe CK, Wood WI, Yan M;
232
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DL, Smith
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RESULT 9 AAY44664

120 89

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149

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Best Loc
Matches
                              Query Match
                                                                        The present sequence is interferon receptor (INFR) HKABF92 encoded by CDNA clone HKABF92 (ATCC No. 209746) derived from human keratinocyte cDNA library. INFR-HKABF92 polypeptides are used in the treatment of disorders associated with viral infection, immune dysfunction and proliferative diseases such as cancer, inflammatory disorders, persistent infection, inflammatory disorders, immunosuppression, inflammatory bowel disease, or myelosuppression. The products can also be activates Jaks-STATS signal transduction pathway in a dose-dependent
                                                  Sequence
                                                                                                                                                                                           Claim 17; Fig 1; 98pp; English.
                                                                                                                                                                                                                                   New
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                                                                                                                                                                                                                      products
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       Local Sim hes 203;
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                                                                                                                                                                                                                                                      2000-147043/13.
DB; AAZ49747.
                  Similarity
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     100.0%; ilarity 100.0%; Conservative 0
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272. .30
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59. .77
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    Score 1080; DB 3;
Pred. No. 9.8e-109;
; Mismatches 0;
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RESULT 10
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                                                                                 Ashkenazi A.
Ferrara N,
Goddard A,
Kljavin IJ,
Stewart TA,
                                                                                                                                                                                           30-NOV-1999;
02-DEC-1999;
02-DEC-1999;
16-DEC-1999;
30-DEC-1999;
30-DEC-1999;
                  target bioa activities.
                         Novel PRO polypeptides and target bioactive molecules
                                                                                                                                                                                                                                                     23-JUN-1999;
26-JUL-1999;
29-OCT-1999;
                                                                                                                                                                                                                                                                                 21-APR-1999;
28-APR-1999;
14-MAY-1999;
                                                       WPI; 2000-611443/58
N-PSDB; AAC78547.
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06-JAN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; secreted protein; transmembrane protein; PRO; EST; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                             expressed sequence tag; detection; cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human
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                                                                                             i AJ, Baker KP,
N, Filvaroff E,
A, Godowski PJ,
IJ, Kuo SS, Nap
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99US-0123957P.

99US-0126773P.

99US-0130232P.

99US-01312445P.

99US-0141037P.

99US-0141037P.

99US-0142698P.

99US-0142698P.

99WO-US028313.

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99WO-US028313.

99WO-US031243.

99WO-US031274.

2000WO-US000276.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UNQ557) protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein;
                                                                                KP, Botstein D, Desnoyers L, Eaton DL;
E, Fong S, Gao W, Gerber H, Gerritse
PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
Napier MA, Pan J, Paoni NF, Roy MA,
Williams PM, Wood WI;
                     polynucleotides used in detection methods, to to specific cells, and to modulate cellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    311
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Gerritsen ME;
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Claim 12; Fig 142; 636pp; English

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RESULT 11
AAY97046
ID AAY97
XX AAY97
XX JAVEN
DE Human
XX TANGG
KW TANGG
KW CYFOCK
KW VIFUC
OS Homo
AX Key
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                                                                                                                                                                                                                                                                                                                                  Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TANGO 242; transmembrane; class II; cytokine receptor; chromosome 3q21; cytostatic; cerebroprotective; immunomodulatory; anti-inflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-OCT-2000.
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                                        WO200039161-A1
                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                                            Domain
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/label=
                                                                                                                                                                        /note= "N-linked glycosylation site"
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                                                                                                                                                note= "N-linked glycosylation
                                                                                                                                                                                                                                  labe1=
                                                                                                                                                                                                                                                                      label=
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                                                                                                                                                                                                                                                            prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cart ear; proliferation; glucose; free fatty acid; skeletal muscle; ad A-peptide; factor VIIA; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  respectively. The proteins, cDNA and their modulators can be used for the treatment of viral and bacterial infection, inflammatory and autoimmune disorders, vascular injury and inhibition of angiogenesis. In particular, TANGO 241 can be used to treat pancreatic disorders and TANGO 242 can be used to treat pancreatic disorders.
01-DEC-1999;
                                                    01-DEC-2000; 2000WO-US032678
                                                                                                                                                                                                                                                                                                                                                                                                                  Human PRO1114 polypeptide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU12187 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 311 AA;
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                                                                                                                                                                                                                         Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 8; Fig 3; 127pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid molecules encoding polypeptides designated TANGO 241 and TANGO 242 used for treating e.g. brain and pancreatic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-DEC-1999;
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DB; AAA51871, A
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Pred. No. 9.8e-109;
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99WO-US031243.
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Isolated , secretory and transmembrane other PRO polypeptides, link bioactive polypeptides, and detect the presence communication of the presence of the prese Gerritsen 2001-408281/43. ₽ AAS21259 ME, Stewart TA, Beresini M, ME, Goddard l A, Godow Tumas D, Deforge L, Desnoyers L, A, Godowski PJ, Gurney ; Tumas D, Watanabe CK, W e PRO polypeptide used to detect e molecules to cells expressing of mammalian tumors e.g. lung, y AL, She wood wI, Filvaroff E, Sherwood ŝ detect Gao Σ

Claim 12; Fig 32; 813pp; English

prostate,

cervical.

PRO

ANUI2172-AAU12446 represent novel human secretory and transmembrane PRO CC polypeptides. The PRO polypeptides are useful to detect other PRO CC polypeptides, to modulate biological activities of cells expressing PRO CC polypeptides, and to detect the presence of mammalian lung, colon, CC press, prostate, rectal, cervical or liver tumours by comparing PRO CC polypeptide expression in a cell sample to that in a control sample. Some CC polypeptide expression in a cell sample to that in a control sample. Some CC polypeptide expression in a cell sample to that in a control sample. Some CC polypeptide expression in a cell sample to that in a control sample. Some CC proliferation of condrocytes, the proliferation or gene expression in CC pericyte cells, the release of proteoglycans from cartilage, the CC proliferation of inner ear utricular supporting cells or of T-CC lymphocytes, the release of a cytokine from peripheral blood monocytes (C PBMCs), or the proliferation of endothelial cells. Some of the PRO CC polypeptides may modulate glucose or free fatty acid uptake by skeletal CC unsecle cells or by addipoytes; or inhibit binding of A-peptide to factor CC UIA. The PRO polypeptides can be used in assays to identify molecules crowled to binding interactions. The polymucleotides encoding PRO Some

The invention relates to an interleukin 20 (II-20) soluble receptor comprising two polypeptide subunits II-20RA (formerly known as ZcytoR7) and II-20RB (formerly known as DRRS1). The two subunits are preferably linked together. In one embodiment, one subunit is fused to the constant region of the light chain of an immunoglobulin, and the other subunit is fused to constant region of the heavy chain of an immunoglobulin. The light chain and the heavy chain are connected via a disulphide bond. The soluble receptor can be used to down-regulate II-20 and thus treat

The invention relates to

Example

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Page

68-69; 119pp;

English.

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RESULT 13
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Best Local S
Matches 203
                                                                                                      Isolated subunits treating
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Rixon MW,
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22-JUN-2000;
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                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                  Interleukin 20; IL-20; IL-20RA; ZcytoR7; IL-20RB; DIRS1; immunoglobulin;
antiinflammatory; antipsoriatic; antiasthmatic; antibacterial; human;
dermatological; antiulcer; antagonist.
                                                                                                                                                                                                                                                                                                                                                                            Human IL-20 receptor subunit IL-20RB
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transgenic or knock out anim
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DB; AAH22816.
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s IL-20RA and I
g inflammatory
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2000US-0213416P.
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                                                                                                             20 soluble receptor comprising two polypeptide IL-20RB, useful for down-regulating IL-20 and
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                                                                                                       diseases such as
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Pred. No. 9.8e-109;
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l can be us
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sed in gene therapy
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Best Local S
Matches 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; cytokine receptor protein; CG92; antiinflammatory; antimicrobial; immunosuppressive; blood coagulation disorder; antidiabetic; cytostatic; gastrointestinal; acute pancreatitis; glomerulonephritis; gene therapy; severe combined immunodeficiency; SCID; autoimmune disorder; thrombosls; multiple sclerosls; rheumatoid arthritis; Alzheimer's disease; kenograft; graft versus host disease; GYHD; inflammatory bowel disease; haemostatic; endotoxin shock; psoriasis; osteoporosis; hepatitis; vascular; allograft; carciagoria; haematopoietic; vasculitis; lupus; leukaemia; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Crohn's
subunit
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                                                                                                                                                                                                                                              Domain
                                                                                                                                                                                                                                                                                             Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human cytokine receptor protein, CG92.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                           Region
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                                                                                                                                                                                        /label= Tissue_factor_domain
235. .255
                                                                                                                              /note= "Shows high homology to sensory transducer signature"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                            note=
                                                                                                                                                                                                                                                                                                                                                                                                                      /label= Mature_human_CG92_protein
                                                                                                                                                                                                                                                                       note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'label= Signal_peptide
                                                                                                                                                                                                                                                                                                                       label= Tissue_factor_signature
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                                                                                                                                                                                                                                                                       "Tissue
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Pred. No. 9.8e-109;
                                                                                                                                                                                                                                                                 factor structure
                                                                                                                                                                                                                                                                                                                                                                            factor structure region"
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                                                                                                                                                            bacterial chemotaxis
                                                                                                                                                                                                                                                                 region"
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The present sequence is human cytokine receptor protein, designated as CC GG92. GG92 is a member of the class II cytokine receptor (CRF2) family, CC which includes R1 and R2 of chains of the II-10 receptor (CRF2) family, CC alpha receptor complex, and tissue factor (TF). GG92 DNA and proteins are CC used in the prevention, diagnosis and treatment of diseases associated CC with inappropriate cytokine receptor expression such as inflammatory CC disorders and disorders of blood coagulation. These disorders include CC sepsis, thrombosis, acute pancreatitis, arthritis, vasculitis, lupus, CC immune complex glomerulonephittis, diabetes, allograft and xenograft CC transplantation, hepatitis, stroke and cancers. It is also used for CC trating various immune deficiencies and disorders such as severe CC combined immunodeficiency (SCID) and autoimmune disorders such as severe CC multiple sclerosis, rheumatoid arthritis; nervous system disorders (e.g., Albheimer's disease); sarcoidosis; leukaemias (e.g., erythroleukaemia); CC inflammations such as graft versus host disease (GVID), inflammatory bowel disease and endotoxin shock; hyperproliferative disorders (e.g., CC pooriasis); cancers (e.g., non-Hodgkin's lymphoma, prostate cancer) and componiesis reculation activity, immune regulating activity. Abamontatic contents in activity tissue growth activity bamontatic
                                                              haematopoiesis regulating activity, tissue growth activity, haemostatic and thromolytic activity, receptor/ligand activity and anti-inflammatory activity. CG92 is also used in assays to identify modulators of cytokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polynucleotides encoding human cytokine receptor CG92, useful preventing, diagnosing and treating inflammation and disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 10; Fig 1-3; 109pp; English.
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                                             receptor expression and their activities
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S 밁 S 문 δ 문 밁 S Query Match Best Local S Matches 203 210 181 150 121 FHLVIELEDLGPQFEFLVAYWRRBPGAEEHVXMVRSGGIPVHLETMEPGAAYCVKAQTFV 203; 90 19 30 Similarity KAIGRYSAFSQTECVEVQGEAIP SLTEGPECDVTDDITATVPYNLRVRATLGSQTSAWSILKHPFNRNSTILTRPGMEITKDG SLTEGPECDVTDDITATVPYNLRVRATLGSQTSAWSILKHPFNRNSTILTRPGMEITKDG DEVAILPAPQNLSVLSTNMKHLLMWSPVIAPGETVYYSVEYQGEYESLYTSHIWIPSSWC DEVAILPAPQNLSVLSTNMKHLLMWSPVIAPGETVYYSVEYQGBYESLYTSHIWIPSSWC FHLVIELEDLGPQFEFLVAYWRREPGAEEHVKMVRSGGIPVHLETMEPGAAYCVKAQTFV Conservative 100.0%; <u>.</u> Score 1080; DB 4; Pred. No. 9.8e-109; ; Mismatches 0; 232 203 Length Indels 311; 0, Gaps 180 149 120 89 209 0

Sequence

311

A A

RESULT 15
AAU04059
ID AAU04
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AC AAU04
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AC AAU04
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XX 23-OCT-2001 AAU04059; AAU04059 standard; (first entry) protein; 311 ጅ

KAIGRYSAFSQTECVEVQGEAIP

Human

interleukin-20 receptor B,

IL-20RB.

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Matches 203;
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence represents the Human interleukin-20 receptor B, IL-20RB. The invention relates to treating a mammal afflicted with a disease in which an interleukin-20 (IL-20) polypeptide plays a role, involves administering antagonist of IL-20 polypeptide to the individual. The method is useful for treating psoriasis, eczema, atopic dermatitis, contact dermatitis, adult respiratory disease, asthma, bronchitis and pneumonia and is also useful for treating multiple organ failure, inflammatory lung injury, septic shock, bacterial pneumonia, inflammatory bowel disease, rheumatoid arthritis, ulcerative colitis and Crohn's
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 311 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Treating interleukin-20 induced inflammation in a mammal, such as adult respiratory disease, eczema, psoriasis, contact dermatitis, multiple organ failure and septic shock, involves administering IL-20 antagonist.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; interleukin-20 receptor B; IL-20RB; antagonist; psoriasis; eczema; dermatitis; adult respiratory disease; asthma; bronchitis; pneumonia; multiple organ failure; inflammatory lung injury; septic shock; bacterial pneumonia; inflammatory bowel disease; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 2; Page 62-63; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAS07644.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-DEC-1999;
22-JUN-2000;
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Sprecher CA,
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                                                                                                                                                                                           SLTEGPECDVTDDITATVPYNLRVRATLGSQTSAWSILKHPFNRNSTILTRPGWBITKDG
                                                                                                                                                                                                                                                                                    DEVAILPAPQNLSVLSTNMKHLLMWSPVIAPGETVYYSVBYQGEYBSLYTSHIWIPSSWC
KAIGRYSAFSQTECVEVQGEAIP 203
                                                                PHLVIELEDLGPOFEFLVAYWRREPGAEEHVKWVRSGGIPVHLETMEPGAAYCVKAQTFV
                                                                                             FHLVIELEDLGPQFEFLVAYWRREPGAEEHVKMVRSGGIPVHLETMEPGAAYCVKAQTFV
                                                                                                                                                                                                                                                       DEVAILPAPONLSVLSTNMKHLLMWSPVIAPGETVYYSVEYQGEYESLYTSHIWIPSSWC
                                                                                                                                                         SLTEGPECDVTDDITATVPYNLRVRATLGSQTSAWSILKHPFNRNSTILTRPGMEITKDG
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                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 1080; DB 4; ilarity 100.0%; Pred. No. 9.8e-109; Conservative 0; Mismatches 0;
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2000US-0213341P.
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Blumberg H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= Mature_IL-20RB
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l, Bagan
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8 8 8 8

210 KAIGRYSAFSQTBCVEVQGEAIP 232

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Search completed: February 25, 2005, 02:39:47 Job time : 121.257 secs

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Listing first 45 summaries
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Perfect score:
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                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                               PIR 79:*
1: pir1:*
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1 DEVAILPAPQNLSVLSTNMK......GRYSAFSQTECVEVQGEAIP 203
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2005 Compugen Ltd.
                                       SUMMARIES
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83 7.7 896 1 82.5 7.6 454 2 82.5 7.6 681 82.5 7.6 716 2 82.5 7.6 1170 2	23	w	7.7	752	N	E72616	
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82.5 7.6 716 2 82.5 7.6 1170 2	26	N	7.6	681	N	839058	
82.5 7.6 1170 2	27	N	7.6	716	N	H85089	
	28	N	7.6	1170	N	I45914	

S67477
B96568
T11053
T11250
T10652
T30938
A33998
JQ1655
A82787
T11483
A54849
A54100
JC5765
S53867

ALIGNMENTS

RESULT 2 JC6311 interferon receptor-class II cytokine receptor - mouse C;Species: Mus musculus (house mouse) C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004 C;Accession: JC6311 R;Gibbs, V.C.; Pennica, D.	Db 25 DPLSQLPÄPQHPKIRLYNAEQVLSWEPVALSNSTRPVVYRVQFKYTDSKWFTADIMSIGV 84 Qy 59 WCSLTEGPECDVTDDITATVPYNLRVRATLGSQTSAWSILKHPFNRNS 106	A; Molecule type: mRNA A; Residues: 1-63,'Q',65-337 <re2> A; Residues: 1-63,'Q',65-337 <re2> A; Cross-references: EMBL:U05877; NID:g463551; PIDN:AAA16956.1; PID:g463552 A; Cross-references: EMBL:U05877; PID:g463551; PIDN:g463551; PIDN:g463552; PID:g463551; PIDN:g463551; PIDN:g463551; PID:g463551; PIDN:g463551; PIDN:g46</re2></re2>	RESULT 1 138500 138500 138500 118510 138500 118510 138500 138501 138501 138501 138501 138501 138501 138502 138501 138502 138503 138503 138503 138503 138503 138503 138503 138503 138503 138504 1, J. Donnelly, R.J.; Kotenko, S.; Mariano, T.M.; Cook, J.R.; Wang, N.; Emanuel, S Cell 76, 793-802, 1994 1, Title: Identification and sequence of an accessory factor required for activation of A; Reference number: A49946; MUID:94170380; PMID:8124716 1, Accession: 138500 1, Accession: 138500 1, PMID:94170380; PMID:8124716 1, PMID:9463549; PIDN:AAA16955.1; PID:9463 1, Cross-references: UNIPROT: P38484; EMBL: U05875; NID:9463549; PIDN:AAA16955.1; PID:9463 1, Accession: 138501 1, Accession: 138501
			anuel, S. tion of PID:g463

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                                                                                                                                                                                                                                                                        A; Map position: 21q; 21q22.1-21q22.2
A; Introns: 17/1; 58/2; 111/1; 166/3; 216/1
                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/E
A;Molecule type: DNA
A;Residues: 1-123,'D',125-268,'VGRME' <LU2>
                                                                                                                                                                                                                                                                                                                                                                                                                                       submitted to the EMBL Data A; Reference number: G06935 A; Accession: G01418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Lutfalla,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-325 < LU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genomics 16, 366-373, 1993
A;Title: A new member of the cytokine receptor gene family maps
A;Reference number: A47003; MUID:93300510; PMID:8314576
A;Accession: A47003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene 186, 97-101, 1997
A;Title: CRP2-4:isolation of cDNA clones encoding the human and mouse proteins. A;Reference number: JC6311; MUID:97199375; PMID:9047351
A;Accession: JC6311
A;Status: preliminary
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A;Residues: 1-349 <GIB>
A;Cross-references: UNIPROT:Q8VHM7; GB:U53696
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                                                                                                                                                                                                                                                                                                          Cross-references: GDB:138168; OMIM:123889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cross-references: UNIPROT: Q08334; GB: Z17227; NID: g393378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Status: preliminary;
                                                                                                                                                                                                      Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                               Gene: GDB:CRFB4; CRF2-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3
                                                                                                                                                                                                      Similarity
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                                  NTTLTECDFS-SLSKYGDHTLRVRAEFADEHSDWVNITFCPV--DDTIIGPPGMQVEVLA 124
                                                                                                                                             VAILPAPQULSVLSTNMKHLLMW-SPVIAPGETVYYSVEYQGEYESLYTSHIWIPSSWCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AESLELRFSAPQIENEPETWTLKNIYDSWAYRVQYWKN--GTNEKFQVVSPYDSEV-LRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HLVIELEDLGPQFE------FLVAYWRREPGAEEHVKMVRSGGIPVHLET 165
   DGFHLVIELEDLGPQFE-
                                                                     LTEGPECDVTDDITATVPYNLRVRATLGSQTSAW-SILKHPFNRNSTILTRPGM--EITK 118
                                                                                                         LGMVPPPENVRMNSVNFKNILQWESPAFAKG----NLTFTAQYLSYR----IFQDKCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LEPWITYCIQVQGFLLDQNRTGEWSEPICERTGNDEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LGMIPPPEKVRMNSVNFKNILQWEVPAFPKTNLTFTAQYE-SYRS-FQDH-----CKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TASTQCDFS-HLSKYGDYTVRVRAELADEHSEWVNVTFCPV--EDTIIGPPEMQI--ESL 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TEGPECDVTDDITATVPYNLRVRATLGSQTSAW-SILKHPFNRNSTILTRPGMEITKDGF 121
                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                         protein
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24.4%; Pred. No. 3.2e-07;
tive 37; Mismatches 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Library,
                                                                                                                                                                                   37;
                                                                                                                                                                                                  Score 159.5; DB Pred. No. 5e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       April 1994
                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                    GB/EMBL/DDBJ
 FLVAYWRREPGAEEHVKMVRSGGIPVH
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162
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Biochim. Biophys. Acta 1173, 314-319, 1993 A;Title: Cloning and characterization of a A;Reference number: S33770; MUID:93305725; A;Accession: S33770
                                                                                                                                                                              A;Cross-references: UNIPROT:Q04790;
A;Experimental source: MDBK cells
R;Lim, J.K.; Langer, J.A.
                                                                                                                                                                                                                                                            A;Title: Specific antiviral activiti
A;Reference number: S27387; MUID:930
A;Accession: S27387
A;Status: preliminary; nucleic acid
A;Molecule type: mRNA
A;Residues: 1-560 <MOU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   interferon alpha receptor type 1 precursor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Hemmi, S.; Bohni, R.; Stark, G.; Di Marco, F.; Aguet, M. Cell 76, 803-810, 1994
A;Title: A novel member of the interferon receptor family complements functionality A;Reference number: A49947; MUID:94170381; PMID:8124717
A;Accession: A49947
                   A;Status: preliminary; nucleic acid A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                       R;Mouchel-Vielh, E.; Lutfalla, G.; Mogensen, K.E.; Uze, FEBS Lett. 313, 255-259, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
A49947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Note: sequence extracted fro C; Keywords: cytokine receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:Q63953; GB:S69336; NID:g545841; PIDN:AAB30165.1; A;Experimental source: early B-cell line Y16
A;Note: sequence extracted from NCBI backbone (NCBIN:145654, NCBIP:145656)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-332 < HEM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Mus musculus (house mouse)
C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              interferon gamma receptor beta subunit - mouse
N;Alternate names: IFN-gamma R beta chain; IFN-gamma R species-specific cofactor;
C;Species: Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Accession: A49947
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65;
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1-421,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ILTRP--GMEITKDGFHLVIELE---DL--GPQFEFLVAYWRREPGAEEHVK-MVRSGGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SITEGPEC-DVTD---DITA----TVPYN--LRVRATLGSQTSAWSILKHPFNRNST 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PVHLETMEPGAAYCVKAQTFV----KAIGRYSAFSQTECVEVQGEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VTVGPPKNISVTPGKGSLVIHFSPPFDVFHGATFQYLVHYWEKSETQQEQVEGPFKSNSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DSFSQLAAPLNPRLHLYNDEQILTWEP--SPSSNDPRPVVYQVEYS-----FIDGSWH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LRNLEPWTTYCVQVRGFLPDRNKAGEWSEPVCEQTTHDETVP 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LETMEPGAAYCVKAQTFVKAIGRYSAFSQTECVE-VQGEAIP 203
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423-560
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                                                                                                                                                                                                                                                                                                                                                                     activities of the human alpha MUID:93076908; PMID:1446745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29;
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Pred. No. 7.1e-07;
                                                 sequence
                                                                                                                                                                                                                                     EMBL: X68443; NID: 9431;
                                                                                                                                                                                                                                                                                                                   sequence
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                                                                                                      bovine alpha
PMID:8318540
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A;Residues: 243-264 <RE3>
A;Cross-references: EMBL:U0
A;Accession: I48426
A;Status: preliminary; tran
A;Molecule type: DNA
A;Residues: 265-375 <RE4>
A;Cross-references: EMBL:U0
A;Accession: I48427
A;Cross-references: EMBL:U0
A;Accession: I49427
A;Status: preliminary; tran
A;Molecule type: DNA
A;Residues: 397-424 <RE5>
A;Cross-references: EMBL:U0
A;Accession: I48428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Mus musculus (house mouse)
C;Sate: 25-Mar-1993 #sequence revision 18-Nov-1994 #text change 09-Jul-2004
C;Accession: A45283; I48423; I48424; I48425; I48426; I48427; I48428; I48429
C;Accession: A45283; I48423; I48424; I48426; I48426; I48427; I48428; I48429
C;Accession: Accession U.S.A. 89, 4774-4778, 1992
A;Title: Behavior of a cloned murine interferon alpha/beta receptor expressed A;Reference number: A45283; MUID:92262522; PMID:1533935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Reference number: 148423; MUID:95047447; PMID:7958966
A;Accession: 148423
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 118-125 <RES>
A;Crose-references: EMBL:U06237; NID:g497103; PIDN:AAA65003.1; PID:g755810
A;Cccssion: 148424
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 127-224 <RES>
A;Residues: 127-224 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ributfalla, G.; Uze, G. Gene 148, 343-346, 1994
A;Title: Structure of the murine interferon alpha/beta receptor-encoding gene: A;Reference number: 148423; MUID:95047447; PMID:7958966
                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:U06238; NID:g497104; PIDN:AAC01749.1; A;ACcession: I48425
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 243-264 <RE3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:L06320; NID:g163187; PIDN:AAA02571.1; PID:g163188 A;Experimental source: lung C;Keywords: antiviral; cytokine receptor; transmembrane protein F;1-24/Domain: signal sequence #status predicted <SIG> F;25-560/Product: interferon alpha receptor type 1 #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Note: sequence
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Matches
                                                                                                                 Status: preliminary; translated
                                                                                                                                                                      Cross-references: EMBL:U06240; NID:g497108;
                                                                                                                                                                                                                                                        Status: preliminary; translated
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                                                                                                                                                                                                                                                                                                               Cross-references: EMBL: U06239; NID: g497106; PIDN: AAA65004.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                282 N -- CENVISTHCVFPREVSSRGIYYVRVRASNGNGISFWSEEKEFNTEMKTIIFPPVISV 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           l Similarity
52; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 LPAPQNLSVLSTNMKHLLMWSPVIAPGETVYYSVEYQGEYESLYTSHI-----W--IP 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KSVTDDSLHVSVGASEESENMSVNQLYPLIYEVIFWENTSNAERKVLEKRTNFI---PPD 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VPSPENIQINADNQIYVLKW------DYPYENATFQAQWLRAFFKKIPGNHSDKWKQIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEPGAAYCVKAQTFVKAIGRY--SAFSQTEC 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSWCSLTEGPECDVTDDITATVPYNLRVRATLGSQTSAWSILKHPFNRNSTILTRPGM-- 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -EITKDGFHLVI----ELEDLGPQ----FEFLVAYWRREPGAEEHVKMVRSGGIPVHLET 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       extracted
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                             EMBL: U06241; NID: 9497110; PIDN: AAA65006.1; PID: 9755812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14.0%; Score 151; DB 2;
24.6%; Pred. No. 6.1e-06;
tive 38; Mismatches 87
                                                                                                                                                                                                                                                           from
                                                                                                                    from
                                                                                                                    GB/EMBL/DDBJ
                                                                                                                                                                                                                                                           GB/EMBL/DDBJ
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                                                                                                                                                                         PIDN: AAA65005.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NID:g194111;
(NCBIN:102354,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIDN:AAA37890.1;
, NCBIP:102357)
                                                                                                                                                                                                                                                                                                               PID:g510261
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PID:g755811
                                                                                                                                                                      PID:g510262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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R;Uze, G.; Lutfalla, G.; Gresser, I.
Cell 60, 225-234, 1990
A;Title: Genetic transfer of a functional human interferon alpha
A;Reference number: A32694; MUID:90124632; PMID:2153461
                                                                                        A;Cross-references: GDB:120078; OMIM:107450
A;Map position: 21922.1-21922.1
A;Introns: 26/1; 67/2; 126/1; 17/3; 225/1; 263/2; 342/1; 381/3; 432/1; 480/3
A;Introns: 26/1; 67/2; 126/1; 17/3; 225/1; 263/2; 342/1; 381/3; 432/1; 480/3
C;Keywords: cytokine receptor; glycoprotein; transmembrane protein
F;1-21/Domain: transmembrane #status predicted <TRN1>
F;437-455/Domain: transmembrane #status predicted <TRN2>
F;50,58,81,88,110,172,254,313,314,376,416,433,507,518,537/Binding site: carbol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    interferon alpha/beta receptor precursor - C;Species: Homo sapiens (man)
C;Date: 22-Jun-1990 #sequence_revision 22-J
C;Accession: A32694; S17112
R;Uze, G.; Lutfalla, G.; Gresser, I.
                                                                                                                                                                                                                                                                                                                                                                                         submitted to the EMBL Data Library, July 1991
A;Description: The structuree of the human interferon alpha/beta receptor A;Reference number: S17112
A;Accession: S17112
                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-16,'A',18-329,'V',343-557 <LUT>
A;Cross_references: EMBL:X60459; NID:g32671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Lutfalla,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-557 < UZE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: A32694
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A;Molecule type: DNA
A;Residues: 426-445 <RE6>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:P17181; GB:J03171; NID:g184645;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNF
A; Residues: 473-590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: I48429
                                                                                                                                                                                                                                                                       ;Gene: GDB:IFNAR1; IFNAR; IFRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;Status: preliminary; translated from GB/EMBL/DDBJ
     Matches
                                                                                                                                                                                                                                                                                                   :Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;Keywords: cytokine receptor; transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Introns: 177/3; 331/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;Gene: IFNAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;Cross-references: EMBL:U06242; NID:g497112; PIDN:AAA65007.1; PID:g755813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                           Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   225-234, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 LPAPQNLSVLSTNMKHLLMWSPVIAPGETVYYSVEYQGEYESLYTSHI--WIPSSWCSLT 63
                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LVYVNCQDSTCDGLNYE--IIFW--ENTSNTKISMEKDGP-EFTLKNLQPLTVYCVQARV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QTTHCVFSQDTVYTGTFFLHVQASEGNHTSFWSEEKFIDSQKHILPPPPVITVTAMSDTL 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MPVPGNLQVDAQGKSYVLKWD-YIASADVLFRAQWLPGYSKSSSGSHSDKWKPIPTCANV 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HLVIELEDL----GPQFEFLVAYWRREPGAEEHVKMVRSGGIPVHLETMEPGAAYCVKAQT 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EGPECDVTDDITATVPYNLRVRATLGSQTSAWSILKHPFNRNSTILTRPGMEIT--KDGF 121
     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL: U06244; NID: g497114; PIDN: AAA65008.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <RE7>
                         12.7%; Score 137.5; DB 2; 22.1%; Pred. No. 0.00011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13.1%; Score 142; DB 2; 24.9%; Pred. No. 4.4e-05;
  37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   194
Mismatches
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     74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95;
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  Indels
                                                Length
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  65;
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  Gaps
                                                                                                  carbohydrate
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Gene 98, 265-269, 1991

A;Title: Conservation of tissue factor primary sequence A;Reference number: JU0441; MUID:91200676; PMID:1840552

A;Accession: JU0441

A;Molecule type: mRNA
A;Residues 1-292 <AND>
A;Cross-references: UNIPROT:P24055; GB:M55390; NID:q1656;
                                                                                                                                          tissue factor precursor - rabbit
N;Alternate names: coagulation factor III
C;Species: Oryctolagus cuniculus (domestic
C;Date: 30-Sep-1993 #sequence_revision 30-
C;Accession: JU0441; S23681
                                                                                                                               R;Andrews, B.S.; Rehemtulla,
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A;Cross-references: GDB:330958; OMIN:146933
A;Map position: 11q23.3-11q23.3
C;Superfamily: interleukin-10 receptor IL10R
C;Keywords: cytokine receptor
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A; Residues: 1-578 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Liu, Y.; Wei, S.H.; Ho, A.S.; de Waal Malefyt, R.; Moore, J. Immunol. 152, 1821-1829, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          interleukin-10 receptor - hum C;Species: Homo Bapiens (man) C;Date: 02-Jul-1996 #sequence C;Accession: I56215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: I56215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Title: Expression cloning A; Reference number: 156215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
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Best Local
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                                                                                                                                                                                                                                                                                                                 194
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                                                                                                                                                                                                                                                                                                                                                                                      141
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                                                                                                                                                                                                                                                                                                                                           RSGGIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECVEV 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PECD-VTDDITATVPYNLRVRATLGSQTSAWSILKHPFNRNSTILT-----
                                                                                                                                                                                                                                                                                                                                                                                  GKIQLPRPKMAPANDTY----
                                                                                                                                                                                                                                                                                                                                                                                                              -----RPGMEITKDGFHLVIELEDLGPQF-EFLVAYWRREPG-----ABEHVKMV 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                  YDLTAVTLDLYHSNGYRARVRAVDGSRHSNWTVTNTRFSVDEVTLTVGSVNLEIHNGFIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LPSPPSVWFEAEFFHHILHWTPIPNQSESTCYEVAL----LRYGIESWNSISNCSQTLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LPAPQNLSVLSTNMKHLLMWSPVIAPGETVYYSVEYQGEYESLYTSHIWIPSSWCSLTEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PFNRNSTILTRPGMEITKDGFHLVI------ELEDLGPQFEFLVAYWRREPGAEEH 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IIEKKT----DVTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVC 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VKMVRSGGIPVHLETMEPGAAYCVKAQ--TFVKAIGRYSAFSQTEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QI----PDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPP 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLITEGPECDVIDDITATVPYN-----LRVRATLGSQTSAWS------ILKH 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LPPPENIEVSVQNQNYVLKW-----DYTYANMTFQVQWLHAFLKRNPGNHLY---KWK 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
       UNIPROT: P24055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UNIPROT: Q13651;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----LSDSFHIYIGAPKQSGNTPVIQDYPLIYE--IIFWENTSNAERK 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and characterization of a human MUID:94165477; PMID:8120391
                                                                                                                                                                                                                                                                                                           -GEFCVQVKPSVASRSNKGMWSKEECISL 226
                                                                                                                           A.; Fowler, B.J.; Edgington,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33;
                                                                                                                                                               (domestic rabbit)
rision 30-Sep-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 122.5; DB 
Pred. No. 0.0027; 
3; Mismatches 8
     GB:M55390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL:U00672; NID:g482802; PIDN:AAA17896.1; PID:g482
                                                                                                                                                                                                                                                                                                                                                                               ESIFSHFREYEIAI-RKVPGNFTFTHKKVKHENFSLL
 NID:g165696; PIDN:AAA63469.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66;
                                                                                                                                                             #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
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                                                                                         among
                                                                                                                       T.S.; Mackman,
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                                                                                         mammalian
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F;250-271/Domain: transmembrane #status predicted <TMM>
F;272-292/Domain: intracellular #status predicted <INT>
F;411.114,154,167,182/Binding site: carbohydrate (Asn) (covalent) #status
F;79-87,216-239/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Keywords: blood coagulation; glycoprotein; lipoprotein; F;1-32/Domain: signal sequence #status predicted <SIG>F;33-292/Product: tissue factor #status predicted <WAT>F;33-249/Domain: extracellular #status predicted <EXTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Experimental source: brain
R;Pawashe, A.; Ezekowitz, M.; Lin, T.C.; Horton, R.; Bach, R
Thromb. Haemost. 66, 315-320, 1991
A;Title: Molecular cloning, characterization and expression
A;Reference number: $23681; MUID:92081032; PMID:1746002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;274/Binding site: palmitate (Cys)
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A;Residues: 33-292 <PAW>
A;Cross-references: EMBL:X53521; NID:g1495; PIDN:CAA37597.1; PID:g3980170
C;Comment: Tissue factor is an integral membrane glycoprotein that serves
C;Comment: Expression of tissue factor can be induced in a variety of tissue factor can be induced in a variety of tissue factor can be induced in a variety of tissue factor can be induced in a variety of tissue factor can be induced in a variety of tissue factor can be induced in a variety of tissue factor can be induced in a variety of tissue factor can be induced in a variety of tissue factor can be induced in a variety of tissue factor can be induced in a variety of tissue factor can be induced in a variety of tissue factor can be induced in a variety of tissue factor can be induced in a variety of tissue factor can be induced in a variety of tissue factor can be induced in a variety of tissue factor can be induced in a variety of tissue factor can be induced in a variety of tissue factor can be induced in a variety of tissue factor can be induced in a variety of tissue factor can be induced in a variety of tissue factor can be induced in a variety of tissue factor can be induced in a variety of tissue factor can be induced in a variety of tissue factor can be induced in a variety of tissue factor can be induced in a variety of tissue factor can be induced in a variety of tissue factor can be induced in a variety of tissue factor can be induced in a variety of tissue factor can be induced in a variety of tissue factor can be induced in a variety of tissue factor can be induced in a variety of tissue factor can be induced in a variety of tissue factor can be induced in a variety of tissue factor can be induced in a variety of tissue factor can be induced in a variety of tissue factor can be induced in a variety of tissue factor can be induced in a variety of tissue factor can be induced in a variety of tissue factor can be induced in a variety of tissue factor can be induced in a variety of tissue factor can be in
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                                                                                                                                                                                                                                                                                                                                                                                                                        84 ETECDLTDEVVKDVGQTYMARVLSYPARNGNTTGFPEEPPFRNSPEFTPYLDTNLGQPTI 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 NLSVLSTNMKHLLMWSPVIAPGETVYYSVEYQGEYESLYTSHI-----WIPSSWCSLTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57;
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                                                                                                                                                                                                                                                                                                   E-ITKDGFHLVIBLED------LGPQFEFLVAYWRREPGAEEHVKMVRS 156
TNTNEFLIDVDKGENYCFSVQAVIPSRKRKQRSPESLTECTSREQGRA
                                                                                               GGIPVHLETMEPGAAYCVKAQTFVKAIGR--YSAFSQTECV-EVQGEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GPECDVTDDITATV--PYNLRVRATLGSQTSAWSILKHPFNRNS-----TILTRPGM 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NLTWKSTNFKTILEWEP-----KSIDH-----VYTVQISTRLENW--KSKCFLTA
                                                                                                                                                                                                         QSFEQVGTKLNVTVQDARTLVRRNGTFLSLRAVFGKDLNYTLYYWR----ASSTGKKTAT
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Pred. No. 0.0036;
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tissue factor precursor [validated] - human N;Alternate names: coagulation factor III C;Species: Homo sapiens (man) C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change C;Accession: A43645; A47574; A28320; A29662; A29672; A2908 A; Molecule type: DNA A; Residues: 1-295 < MAC> A;Title: Complete sequence of the human tissue factor gene, A;Reference number: A43645; MUID:89247359; PMID:2719931 A;Accession: A43645 R;Mackman, N.; Morrissey, J.H.; Fowler, B.; Edgington, Biochemistry 28, 1755-1762, 1989 ø highly 09-Jul-2004 regulated

cellular

A;Cross-references: UNIPROT:P13726; (R;Fisher, K.L.; Gorman, C.M.; Vehar, Thromb. Res. 48, 89-99, 1987 GB:J02846; NID:g339505; PIDN:AAA61152.1; G.A.; O'Brien, D.P.; Lawn, R.M. PID: 933950

A; Title: Cloning and expression of human tissue factor cDNA A; Reference number: A47574; MUID:88100453; PMID:3424286

A; Accession: A47574

A;Molecule type: mRNA
A;Residues: 1-295 <FIS:NA
A;Residues: 1-295 <FIS:NA
A;Residues: 1-295 <FIS:NA
A;Cross-references: GB:M27436; NID:g339507; PIDN:AAA36734.1; PID:g339508
A;Spicer, E.K.; Horton, R.; Bloem, L.; Bach, R.; Williams, K.R.; Guha, A.
Proc. Natl. Acad. Sci. U.S.A. 84, 5148-5152, 1987
A;Title: Isolation of cDNA clones coding for human tissue factor: primary
A;Reference number: A94171; MUID:87260946; PMID:3037536
A;Accession: A28320 Α.;

Kraus,

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factor: primary structure

mRNA

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A; Map position: 1922-1921
A;Introns: 34/1; 71/2; 138/1; 197/3; 251/1
C;Superfamily: tissue factor
C;Kuywords: blood coagulation; glycoprotein; lipoprotein; thiolester bond; transmembrane
F;1-32/Domain: signal sequence #status predicted <SIG>
F;33-295/Product: tissue factor #status experimental <MAT>
F;33-295/Product: tissue factor #status predicted <EXT>
F;33-295/Product: tissue factor #status predicted <TMY>
F;25-274/Domain: extracellular #status predicted <TMY>
F;275-295/Domain: transmembrane #status predicted <INT>
F;43/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;61-89,218-241/Disulfide bonds: #status experimental
F;156,169/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;277/Binding site: palmitate (Cys) (covalent) #status experimental
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A; Residues: 1-259, 'A', 261-295 <SCA>
A; Residues: 1-259, 'A', 261-295 <SCA>
A; Cross-references: GB:M16553; NID:g339503; PIDN:AAA61151.1; PID:g339504
R; Bach, R.; Konigsberg, W.H.; Nemerson, Y.
Blochemistry 27, 4227-4231, 1988
Blochemistry 27, 4227-4231, 1988
A; Title: Human tissue factor contains thioester-linked palmitate and stearate of the second party and the second party and the second party acid binding site
C; Comment: annotation; disulfide bonds and fatty acid binding site
C; Comment: Tissue factor is an integral membrane glycoprotein that serves as a C; Comment: Expression of tissue factor can be induced in a variety of tissues b
                                                                                                                                                                                                       RESULT
A49667
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A;Cross references: GB:J02931; NID:g339501; PIDN:AAA61150.1; PID:g339502
A;Note: part of this sequence, including the amino end of the mature protein, was confi.
R;Scarpati, E.M.; Wen, D.; Broze Jr., G.J.; Miletich, J.P.; Plandermeyer, R.R.; Siegel,
Biochemistry 26, 5234-5238, 1987
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A;Title: Molecular cloning of the cDNA for tissue factor, A;Reference number: A29062; MUID:87244317; PMID:3297348
R;HO, A.S.; Liu, Y.; Khan, T.A.; Hsu, D.H.; Bazan, Proc. Natl. Acad. Sci. U.S.A. 90, 11267-11271, 199; A;Title: A receptor for interleukin 10 is related
                                                                                          interleukin-10 receptor - mouse
c;Speciles: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: A49667
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A;Title: Human tissue factor: cDNA sequence and chromosome localization of the A;Reference number: A29672; MUID:88050796; PMID:2823875
A;Accession: A29672
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                                                                                                                                                                                                                                                                                                                             NEFLIDVDKGENYCFSVQAVIPSRTVNRKSTDSPVECMGQEKGE 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDVTDDITATV--PYNLRVRATLGSQTSAWSILKHPFNRNS-----TILTRPGME-I 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APQNLSVLSTNMKHLLMWSPVIAPGETVYYSVEYQGEYESLYTSHIWIPSSWCSLTEGPE
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Fakhrai, H.; Edgington, T.S.
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      to interferon
                                                            J.F.; Moore,
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A;Reference number: A49667; MUID:94068585; PMID:8248239
A;Accession: A49667
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-575 <RES>
A;Cross-references: UNIPROT:Q61727; GB:L12120; NID:g4376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Superfamily: tissue factor
C;Keywords: blood coagulation; glycoprotein; lipoprotein; thiolester bond; transmembran
C;Keywords: blood coagulation; glycoprotein; lipoprotein; thiolester bond; transmembran
F;16-155/Domain: signal sequence #status predicted <SIG>
F;36-292/Product: tissue factor #status experimental <MAT>
F;36-292/Product: tissue factor #status predicted <EXT>
F;36-248/Domain: extracellular #status predicted <EXT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biochem. Biophys. Res. Commun. 181, 1145-1150, 1991
A,Title: CDNA and amino acid sequences of bovine tissue
A;Reference number: JQ1319; MUID:92109720; PMID:1764065
A;Accession: JQ1319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;249-271/Domain: transmembrane #status predicted <TMM>
F;272-292/Domain: intracellular #status predicted <INT>
F;272-292/Domain: intracellular #status predicted <INT>
F;473,153,181/Binding site: carbohydrate (Asn) (covalent) #status
F;81-89,215-238/Disulfide bonds: #status predicted
F;118,124/Binding site: carbohydrate (Thr) (covalent) #status predicted
F;274/Binding site: palmitate (Cys) (covalent) #status experiment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Experimental source: adrenal gland
A;Note: part of this sequence, including the amino end of the mature protein, was confi
C;Comment: Tissue factor is an integral membrane glycoprotein that serves as a receptor
C;Comment: Expression of tissue factor can be induced in a variety of tissues by certai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Accession: JQ1319
R; Takayenoki, Y.; Mu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N; Alternate names: coagulation factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 12
KFB03
KFB03
tissue factor precursor - bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-292 <TAK>
A;Cross-references: UNIPROT:P30931;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;Species: Bos primigenius taurus (cattle);Date: 30-Sep-1993 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gene: Illor
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                     44;
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                                                                                                                    TKDGFHLVIELED---
                                                                                                                                                                                                                                      GPECDVTDDITATVPYNLRVRATLGSQTSAWSILKHPFNRN-----STILTRPGME-I 116
                                                                                                                                                                                                                                                                                                NITWKSTNFKTILEWEP----
                                                                                                                                                                                                                                                                                                                                                       NLSVLSTNMKHLLMWSPVIAPGETVYYSVEYQGEYESLYTSHI-----WIPSSWCSLTE 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Y.; Muta, T.; Miyata,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LSCOLTTFTLDLYHRSYGYRARVRAVDNSOYSNWTTTETRFTVDEVILT
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PVHLETMEPGAAYCVKAQTFV--KAIGRYSAFSQTEC
                                                                                                                                                                              NTECDVTDEIVKNVRETYLARVLSYPADTSSSTVEPPFTNSPEPTPYLETNLGQPTIQSF 145
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                                                          EQVGTKLNVTVQDARTLVRANSAFLSLRDVFGKDLNYTLYYWKASSTGKKKATTNTNG--
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                                                                                                                                                                                                                                                                                                                                                                                                               Score 103; DB 1;
Pred. No. 0.07;
1; Mismatches 88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GB:S74147; NID:g241438; PIDN:AAB20755.1; PID:g24143
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                                                                                                                 -LGPQFEFLVAYWRREPGAEEHVKMVRSGGI 159
                                                                                                                                                                                                                                                                                             -- KPINHVYTVQISPRLGNW--KNKCFYTT
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C;Accession: A49724
R;Matozaki, T.; Suzuki, T.; Uchida, T.; Inazawa, J.; Ariyama, T.; Matsuda, K.; Horita, J. Biol. Chem. 269, 2075-2081, 1994
A;Title: Molecular cloning of a human transmembrane-type protein tyrosine phosphatase A;Reference number: A49724; MUID:94124561; PMID:8294459
A;Accession: A49724
                                                                                                                                                                                                        protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type H precursor - hum N; Alternate names: protein-tyrosine-phosphatase, stomach cancer-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:M57896; GB:U05713; NID:g201926; PIDN:AAA63400.1; PID:g201927
A;Note: 26-Thr was also found
C;Comment: Tissue factor is an integral membrane glycoprotein that serves as a receptor C;Comment: Expression of tissue factor can be induced in a variety of tissues by certain C;Superfamily: tissue factor
C;Superfamily: tissue factor
C;Keywords: blood coagulation; glycoprotein; lipoprotein; thiolester bond; transmembrane F;11-29/Domain: signal sequence #status predicted <SIG>F;10-294/Product: tissue factor #status predicted <MAT>
C:10-294/Product: tissue factor #status predicted <MAT>
            A; Molecule type:
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A;Title: Cloning of murine tissue factor and regulation A;Reference number: A39046, MUID:91093171; PMID:1985911 A;Accession: A39046
A;Molecule type: mRNA
A;Residues: 1-25, /1, 27-294 <RAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;252-274/Domain: transmembrane #status predicted <TMM>
F;37,57,169,200/Binding site: carbohydrate (Asn) (covalent) #status
F;75-83,218-241/Disulfide bonds: #status predicted
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J. Biol. Chem.
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A;Title: A growth factor-responsive gene of murine BALB/c 3T3 cells
A:Reference number: A32318; MUID:89343974; PMID:2761539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tissue factor precursor - mouse
N,Alternate names: coagulation factor III
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
C;Accession: A32318; A39046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:P20352; GB:M26071; NID:g201924; PIDN:AAA40414.1; R;Ranganathan, G.; Blatti, S.P.; Subramaniam, M.; Fass, D.N.; Maihle, N.J.; (J. Biol. Chem. 266, 496-501, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-294 <HAR>
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Best Local S
Matches 54
                                                                                                                                                               Date: 03-May-1994 #sequence_revision
                                                                                                                                                                                                    ;Species: Homo sapiens (man)
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                                                                                                                                                                                                                                                                                                                                                       ITNTNEFSIDV-----EEGVSYCFFVQAMIFSRKTNONSPGSSTVCTE 243
                                                                                                                                                                                                                                                                                                                                                                                                   VKMVRSGGIPVHLETMEPGAAYC--VKAQTFVKAIGRYSAFSQTECVE 196
                                                                                                                                                                                                                                                                                                                                                                                                                                               GQPVIQQFEQDGRKLNVVVKDSLTLVRKNGTFLTLRQVFGKDLGYIITYRKGSSTGKKTN
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23.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                               23-Feb-1996 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -SRNW--KNKCFSTTDTECD
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Getz, M.J.
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tumor suppressor - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change
C;Accession: I51669
R;Pierceall, W.E.; Reale, M.A.; Candia, A.F.; Wright, C.V.; Cho, Dev. Biol. 166, 654-665, 1994
                                                                                                                                                                                                                                                                                                              A; Gene:
                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-1427 < PIE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Title: Expression of a homologue of the A; Reference number: I51668; MUID: 95113183; A; Accession: I51669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;116-199/Domain: fibronectin type III repeat homology <3FNB>
F;205-289/Domain: fibronectin type III repeat homology <3FNC>
F;296-379/Domain: fibronectin type III repeat homology <3FNC>
F;385-468/Domain: fibronectin type III repeat homology <3FND>
F;385-468/Domain: fibronectin type III repeat homology <3FNE>
F;474-558/Domain: fibronectin type III repeat homology <3FNF>
F;564-658/Domain: fibronectin type III repeat homology <3FNG>
F;667-737/Domain: fibronectin type III repeat homology <3FNG>
F;667-737/Domain: transmembrane #status predicted <INN>
F;762-778/Domain: intracellular #status predicted <INT>
F;767-1118/Domain: intracellular #status predicted <INT>
F;767-1118/Domain: intracellular #status predicted <INT>
F;779-1118/Domain: intracellular #status predicted <INT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;846-1070/Domain: protein-tyrosine-phosphatase homology <PTP1>
F;35.78,83,107,132,149,172,196,203,286,304,312,329,352,376,383,401,436,439,470,490,558,5
F;1022/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1028/Binding site: substrate phosphate (Arg) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;28-761/Domain: extracellular #status predicted <EXT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Map position: 19q13.4-19q13.4 A; Map position: 19q13.4 A; Map position
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references:
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references:
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                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                 Genetics
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                                                                                                                                                         Local
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                                                                                                                                                                                                                                                                                                              XDCCa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143 REPGAEEHVKMVRSGGI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            103 NRNSTILTRPGMEITKDG-----FHLVIELEDLGPQFEFLVAYW---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93
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               9
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                                                                                                                                                    Similarity
PONLSVLSTNMKHL-LMWSPVIAPGETVYYSVEY-----QGEYESLYTSHIWI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLYTCSVWVEK-----DGVNSSVGTVTTATAPNPVRNLRVEAQTNSSIALTWEVPDGPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NATTAHNPVRKPESGGSDHQLHLPELGGPRWHRPTELDLLRTSALEMVAEQRLETQQTPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PQNSTY----GVEYTGDGGRAGTRSTAHTNITVDGLEPGCLYAFSMWVGKNGINSSRETR
                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                UNIPROT: Q91562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UNIPROT:Q15426; GB:D15049; NID:g475003; PIDN:BAA03645.1; PID:g475004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GDB:305504
                                                                                                                                                    8.3%;
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                                                                                                                                                    Score 89.5;
Pred. No. 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from
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Pred. No. 0.53;
                                                                                                                                                                                                                                                                                                                                                                                      EMBL:U10986; NID:g606873; PIDN:AAA70168.1; PID:g606
                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 deleted in colorectal; PMID:7813784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----PVHLETMEPGAAYCVKAQTF-----
                                                                                                                                               .2
                                                                                                                                                                                                       BB
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                                                                                                                                                                                             Length 1427;
                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1118;
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                                                                                                 81;
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Search completed: Febru Job time : 25.4599 secs						
)mplet : 25.	775	155	745	95	685	56
ed: F 4599	DSKQR	RSGGI	MT	WSILK	GLEKG	
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ry 25,	NLEPS	IMEPG	NIV	NSTIL	QVAAM	
Search completed: February 25, 2005, 02:45:39 Job time : 25.4599 secs	SIENLEPSSHYVISLKAFI	AYCVK	745 WTPPLNPNIVVR	TR PGME	TVNGTG	
02:	: LKAFN	AQTEV		ITKDG	PSSDW	PSSWC
45:39	775 DSKQRYYSIENLEPSSHYVISLKAFNNA	155 RSGGIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECVEVQGEAIP 203	-	95 WSILKHPPNRNSTILTRPGMEITKDGFHLVIELEDLGPQFEFLVAYWRREPGAEEHVKWV 154	685 GLEKGSQYSFQVAAMTVNGTGPSSDWYTAETPENDLDESQVPDQPSSLHVRPLTTSIIMS 744	PSSWCSLTEGPECDVTDDITATVPYNLRVRATLGSQTSA 94
		(SAFSC		STEDIC	ETPENDLDESQVPDQPSSLHVR	ECDVI
		TECVE	GY	; PQFEF	: ESQVP	ATIDO
	GEGVP 807	VQGEA:	GYIIGYGVGSPYAETVRV 774	LVAYWI	DQPSSI	TVPYNI
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		_	ETV	EEHVK	TTSII	TGSQT
			RV 7	-¥	MS 7	SA 9
			74	54	44	4

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Result
No.
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Listing first 45 s
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Maximum DB seq length: 200000000
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OM protein - protein search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence:
      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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2: uniprot_trembl:*
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110S HUMAN
Q98UU4
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Q659J5
INR1 BOVIN
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Q8iyy5 homo
P38484 homo
Q9pyj9 gallu
Q9yhw0 gallu
Q96a41 homo
Q61190 mus m
 Q6uwml
Q6uyml
Q04790
Q07zt26
Q04790
Q7zt26
Q09uhf4
Q6phb0
Q72st39
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Q9buu4
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Q78ec1
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                6 mus musculu
5 xenopus lae
8 mus musculu
5 tetraodon n
1 homo sapien
2 homo sapien
2 sus scrofa
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homo sapien
yallus gall
gallus gall
lomo sapien
mus musculu
homo sapien
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mouse CDNA s	neration and	ceriteld Y.S.	riguez A.C.,	keslev R.W.,	ey J., Helton	lalon D.K., M	barda S. Wor	a S.S., Loque	wnstein M.J.,	pleton M., So	kina R.F., Jo	schul S.F., Z	usner R.D., C	LINE=22388257 Ansberg R L	SUB=Cervix, a	SEQUENCE FROM N.A. (ISOFORMS 1	ome Res. 13:2	informatics a	e secreted pr	owski P., Gra	dien R., Wata	Seshagiri S., Si	is L., Liao D	on D., Foster	n J., Chow B.	LINE=22887296 rk H.F., Gurn	UENCE FROM N.	NCBI_TaxID=9606;	aryota; Metaz malia: Futher	o sapiens (Hu	Q55//PROLITY) e=IL20RB: Syn	erleukin-20 r	OCT-2004 (Rel JAN-2005 (Rel	OCT-2004 (Rel	I20S HUMAN STANDARD;	AN		11.	2.5 11.	5.5 11. 123 11.	6.5 11.	5 11.	128 11.	ωυ	135 12.	6 12.	
equences.";	initial ana	N., Krzywin	Grimwood J.	n A., roung Touchman J.	E., Kettem	uzny D.M.,	lev K.C. H	llano N.A.,	Usdin T.B.	ares M.B.,	rdan H., Mo	eeberg B.,	olling F.S.	57; PubMed=1247	nd Skin;	A. (ISOFORM	265-2270 (20	ssessment."	ed protein discove	у A. ;	Watanabe C., Wi	Simmons L., S	Mark M.,	Grima	н с.,	oMed≕1:	ISOFOR		oa; Chordata	man).	lonvms=DIRS1	eceptor bet	. 45, Last	at	TANDARD;			578 1 336 2	333 2	338 2 209 2	521 2	520 2	560 2	341 2	508 2	590 2 508 2	
	"Generation and initial analysis of more than 15,000 full	ones S.T.M. Ma	, Schmutz J., M	W. Green E.D.	an M., Madan A.	Sodergren E.J.,	ale S. Garcia	Peters G.J., A	Toshiyuki S.,	Bonaldo M.F., C	Farmer A A B	Buetow K.H., Sc	, Wagner L., Sh	477932; DOI=10.		S 1 AND 2).	03).		y initiati	9 / 21.00.9 4	eand D., Woods	ingh J., Smith	Robbie E., San	di C., Gu Q., H	Crowley C., Cur	1=12975309; DOI=10.1101/gr.12! , Abaya E., Baker K., Baldwin	1).		i; Craniata;		•	a chain precursor	sequence update annotation upda	.ed)	PRT; 311 AA		ALIGNMENTS	I10R_HUMAN Q800E8	Q7ZT30	Q800G2 Q96SH7	06ZML8	Q81218 Q81U57	Q764M8	09YGC8	Q9PVK0	Q80UJ3 Q6QIU4	
2000		Ka U., Smailus D.E.	•	c	Sa		A M Gay I J Hillyk	bramson R.D., Mulla	Carninci P., Prange C	asavant T.L., Schee	., Wang J., Heich I	at	ule	10.1073/pnas.242603899				ת נימווסווופווהדמוופ היסנ	(SPDI), a large-		Goddard A. Wood W	ons L., Singh J., Smith V., Stinson J., Vagts 1	chez C., Schoenfeld	ass P.E., Heldens S	uel	មន្ត		5	Eutel			(IL-20R-beta)	te)	•	A.			Q13651 Q800e8	Q7zt30	Q800g2 Q96sh7	Q6zml8	Q81218 Q81u57	Q764m8	09 yg c8	Q9pvk0	Q80uj3 O6giu4	
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

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Genew; E. IP
                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entre the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                            Biochemistry 42:12617-12624(2003).

-I-FUNCTION: The IL20RA/IL20RB dimer is a receptor for IL19, IL20 : IL24. The IL22RA1/IL20RB dimer is a receptor for IL20 and IL24.
-I-SUBUNIT: Heterdimer with IL20RA and heterodimer with IL22RA1.
-I-SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
-I-ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WIodawer A., Zdanov A.;
"Characterization of the recombinant extracellular domains of human
interleukin-20 receptors and their complexes with interleukin-19 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SÜBUNIT, LIGAND BINDING, AND TISSUB SPECIFICITY.

MEDLINB=21097717; PubMed=11163236; DOI=10.1016/S0092-8674(01)00187-8;
Blumberg H., Conklin D., Xu W.F., Grossmann A., Brender T.,
Carollo S., Eagan M., Foster D., Haldeman B.A., Hammond A., Haugen H.,
Jelinek L., Kelly J.D., Madden K., Maurer M.F., Parrish-Novak J.,
Prunkard D., Sexson S., Sprecher C., Waggie K., West J.,
Whitmore T.E., Yao L., Kuechle M.K., Dale B.A., Chandrasekher Y.A.,
"Interleukin 20: discovery, receptor identification, and role in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complexes. Differences in receptor-ligand biological functions.";
J. Biol. Chem. 277:47517-47523 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT, AND LIGAND BINDING.
PubMed=12351624; DOI=10.1074/jbc.M205114200;
Parrish-Novak J., Xu W., Brender T., Yao L., Jones C., West J
Brandt C., Jelinek L., Madden K., McKernan P.A., Foster D.C.,
Jaspers S., Chandrasekher Y.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Signal F
verified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 30-44 (ISOFORM 1).
PubMed=15340161; DOI=10.1110/ps.04682504;
Zhang Z., Henzel W.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [3]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=14580208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Interleukins 19, 20, and 24 signal through two distinct receptor complexes. Differences in receptor-ligand interactions mediate un
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Immunol. 167:
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PubMed=11564763;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein
                                                                                                                                                                                                                                 IsoId=Q6UXLO-2; Sequence=VSP_011499, VSP_011500; TISSUB_SPECIFICITY: Widely expressed with highest levels and testis. Highly expressed in psoriatic skin.
SIMILARITY: Belongs to the type II cytokine family of rec SIMILARITY: Contains 2 fibronectin type III domains.
                                                                                                                                                                                                                                                                                                                                                                Event=Alternative
                                                                AY358305;
BC027449;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         104:9-19(2001).
                                                    BC063696;
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                                HGNC:6004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                peptide prediction based
d cleavage sites.";
Sci. 13:2819-2824(2004).
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AND LIGAND BINDING.

RO21/bi0354583;

Kozlov S., Tobin
    IPR000282;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ation by IL-19, IL-20 f two types."; 167:3545-3549(2001).
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                                              ; AAQ88672.1; -.
; AAH27449.1; -.
; AAH63696.1; -.
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Cytok_receptor_2
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RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buecow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
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01-MAR-2003
01-MAR-2003
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TRANSMEM
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Mammalia; Eutheria;
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Homo sapiens (Human)
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01-MAR-2003 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
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IPR008957;
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Fibronectin type-III 2.
Fibronectin type-III 2.
By similarity.
N-linked (GlcNAc. .) (
N-linked (GlcNAc. .) (
Missing (in isoform 2 ar
                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
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/FTId=VSP 011499.
Missing (In isoform 2
/FTId=VSP_011500.
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Cytoplasmic
                                                                                                                                                                                                                                                       Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1080; DB 1;
Pred. No. 8.3e-94;
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(Potential).
and isoform 3)
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Best Local (
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Gazcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Lung fibroblast;

MBDLINE=94170380; PubMed=8124716; DOI=10.1016/0092-8674(94)90354-9;

Soh J., Donnelly R.J., Kotenko S., Mariano T.M., Cook J.R., Wang N.,

Emanuel S.L., Schwartz B., Miki T., Pestka S.;

"Identification and sequence of an accessory factor required for activation of the human interferon gamma receptor.";

Cell 76:793-802(1994).
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01-OCT-1994 (Rel. 30, Last sequence update)
05-ULL-2004 (Rel. 44, Last annotation update)
Interferon-gamma receptor beta chain precursor (Interferon-gamma receptor accessory factor-1) (AP-1) (Interferon-gamma transducer-1).
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GO; GO:0016020; C:membrane; IEA.
GO; GO:001696; F:hematopoietin/interferon-class Interfero; IPR000282; Cytok receptor 2.
Interfero; IPR000957; FN III-1ike. -
SEQUENCE 147 AA; 16945 MW; 71BAF49274618999 C
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens (Human)
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Krzywinski M.I., Skalska U.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SSUE=Skin;
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c. Natl. Acad. Sci. U.S.
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Smailus
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Pred. No.
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D.B., Schnerch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      337
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VARIANT
                                                                                                                                                                                                                  InterPro; IPR000282; Cyrok receptor 2.
InterPro; IPR003961; FN III.
InterPro; IPR008957; FN_III-like.
Pfam; PF00041; fn3. 1
                                                                                                                                 TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glycoprotein;
SIGNAL
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EMBL; U05877; AAA16956.1; -.
                                                                                                                                                                                                                                                                   88888
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                                                                                                                                                                                                                                                                                                                                                       Genew; HGNC:5440; IF
H-InvDB; HIX0016076;
                                                                                                                                                                                                                                                                                                                                                                                          EMBL; BC003624; AAH03624.1; -. EMBL; U68755; AAC52066.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=97067142; PubMed=8910544; DOI=10.1074/jbc.271.46.28947; Rhee S., Ebensperger C., Dembic Z., Pestka S.; The structure of the gene for the second chain of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley M., Madan J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska M.S., Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                      Pfam; PF00041; fn3; 1. PROSITE; PS50853; FN3; 2.
                                                                                                           DOMAIN
                                                                                                                       DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mouse cDNA sequences."
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248
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2319
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                                                                                                                                                                                                                                                                 C:integral to plasma membrane; TAS.
P:interferon-gamma receptor activity; TAS.
P:cell surface receptor linked signal tran
P:response to pathogenic bacteria; TAS.
P:response to virus; TAS.
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                       337
247
2268
337
129
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2110
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2319
 37834
                                                                                                                                                                                          Repeat; Signal;
 ¥;
                               Cytoplasmic (Potential).
Fibronectin type-III 1.
Fibronectin type-III 2.
N-linked (GlcNAc...) (
                                                                                                                                             Potential
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/FTId=VAR_002718.
18C61B10AD90E509
                                                                                                                                                                     -gamma
                                                                                                                                                                                             Transmembrane
                                                                                                                                   (Potential).
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 CRC64;
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d is likely to
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(Potential).
(Potential).
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(Potential).
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Query Match Best Local S Matches 64

Similarity

28.2%; 16.0%;

Score 173; DB Pred. No. 6.7e 31; Mismatches

6.7e-08

DB 1;

Length 337;

Indels

36;

Gaps

11;

Conservative

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RESULT 4
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Best Local
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01-MAY-2000
01-MAY-2000
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EMBL; AF082667; AAD13679.1; -.
GO; GO:0016020; C:membrane; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. ..; GO; GO:0004872; F:receptor activity; IEA.
InterPro; IPR000282; Cytok receptor_2.
InterPro; IPR003961; FN III.
InterPro; IPR003961; FN III.
InterPro; IPR008957; FN III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ol-MAY-2000 (TrEMBLrel. 13, Created)
Ol-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Ol-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Interferon alpha/beta receptor 1 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          receptor gene cluster.";
Genome Res. 9:242-250(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=99177346; PubMed=10077530;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE;
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QTIATVSDLAPSTLYCVKVQAFSEAYNKSSDFSREECIGTAG
                                                                                                                                                                                                                                                                                  LPAPQNLSVLSTNMKHLLMWSPVIAPGETVYYSVEY-QGEYESLYT--SHIWIPSSWCSL
                                      GIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECVEVQG
                                                                                                                     LKHPFNRNSTILTRPGMEITKDGFHLVIELEDLGPQFEFLVAYWRREPGAEEHVKMVRSG
                                                                                                                                                           ITSMKCNLSSVIKPTSASYYFRVQAMNEYNKSCLSKDVEVDPPVTNEIGPPDVKVDISDV
                                                                                                                                                                                                   TEGPECDVTDDITAT-VPYNLRVRATLGSQTSAWS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               I--SLDNLKPSRVYCLQVQAQLLWNKSNIFRVGHLSNISCYETMADA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TVGPPENIEVTPGEGSLIIRFSSPFDIADTSTAFFCYYVHYW--EKGGIQQVKGPFRSNS 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEVAILPAPQNLSVLSTNMKHLLMWSPVIAPGET--VYYSVEYQGEYESLYTSHIWIPSS
                                                                                                                                                                                                                                            LLCPTNVRVFALNMKFYLLWDNHY--NEHVTYTVQYLTGYLKNLYDDYSSKWQKVSGCEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     I PVHLETMEPGAAYCVKAQTFV----KAIGRYSAFSQTECVEVQGEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCTQITATEC----DFTAASPSAGFPMDFNVTLRLRAELGALHSAWVTMPWFQH--YRNV 138
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442 j
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                                                                                                                                                                                                                                                                                                                                                                                                                                 442
                                                                                                                                                                                                                                                                                                                                                                                                              49877 MW;
                                                                                                                                                                                                                                                                                                                                                16.0%;
                                                                                                                                                                                                                                                                                                                             27;
                                                                                                                                                                                                                                                                                                                           Score 173; DB 2; I
Pred. No. 9.3e-08;
7; Mismatches 91;
                                                                                GPGNKIMSDLYD
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interferon/interleukin-10
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RESULT

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DT 05-J
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Genome Res. 9:242-250(1999).
EMBL; AF08264; AAD11569.1;
GO; GO:0016020; C:membrane; IEA.
GO; GO:0004996; F:hematopoletin/Interferon-class (D:GO:0004976; F:receptor activity; IEA.
InterPro; IPR000282; Cytok_receptor_2.
InterPro; IPR003561; FN III.
InterPro; IPR003597; FN III.
                                                                                                                                                                                                                                                                                                          Q96A41 PRELIMINARY; 2...,
Q96A41;
Q96A41;
O1-DEC-2001 (TrEMBLrel. 19, Created)
O1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
O5-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Soluble cytokine class II receptor, short isoform precursor
Soluble cytokine class II receptor, short isoform precursor
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Q9YHW0;
01-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Receptor.
SEQUENCE
   SEQUENCE FROM N.A.
TISSUE=Mammary gland;
MEDLINE=21518574; Pub
                                                                                                                                                                     Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                          Name=CRF2-S1; Synonyms=IL-22BP, IL22BP, IL22RA2; ORFNames=UNQ5793;
                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=IFNAR1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS50853; FN3; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=99177346; PubMed=10077530;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Archosauria; Aves; Neognathae; Galliformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Interferon alpha/beta receptor 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     237 LLCPINVRVFALNMKFYLLMDNHY--NEHVTYTVQYLTGYLKNLYDDYSSKWQKVSGCEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECVEVQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLH-----IKITPPG----GPGNKIMSDLYD----FSYQILYWKNSSDNEEEVKMKETK 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LKHPFNRNSTILTRPGMEITKDGFHLVIELEDLGPQFEFLVAYWRREPGAEEHVKMVRSG
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PubMed=11607789; DOI=10.1038/sj.gene.6363786;
                                                                                                                                                                            Primates;
                                                                                                                                                                                                        Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64055 MW;
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27.0%;
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Pred. No.
                                                                                                                                                                     Craniata; Vertebrata; Catarrhini; Hominidae
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interferon/interleukin-10
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                                                                                                                                                                        Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91;
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                                                                                                                                                                                                           Euteleostomi;
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Best Local Similarity
Matches 57; Conser
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Genome Res. 13:2265-2270(2003).
EMBL; AJ313161; CAC85634 1; --
EMBL; AJ297262; CAC83097.1; --
EMBL; AY040566; AAK85714.1; --
EMBL; AY040428; AAK91775.1; --
EMBL; AY044429; AAK9178.1; --
EMBL; AY044429; AX94849; AY049; AY0
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=21366522; PubMed=11481447; DOI=10.1073/pnas.171303198;

XU W., Presnell S.R., Parrish-Novak J., Kindsvogel W., Jaspers S.,

Chen Z., Dillon S.R., Gao Z., Gilbert T., Madden K., Schlutsmeyer

Yao L., Whitmore T.B., Chandrasekher Y., Grant F.J., Maurer M.,

Jelinek L., Storey H., Brender T., Hammond A., Topouzis S.,

Clegg C.H., Foster D.C.;

"A soluble class II cytokine receptor, IL-22RA2, is a naturally

occurring IL-22 antagonist.";

Proc. Natl. Acad. Sci. U.S.A. 98:9511-9516(2001).
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MEDLINB-22887296; PubMed-12975309; DOI=10.1101/gr.1293003;

Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,

Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,

Chen J., Chow B., Chui C., Crowley C., Currell B., Doud P.

Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,

Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,

Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,

Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,

Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,

Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
                                                                                                                                                                                                                                                                                                                                                                                 Receptor;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Breast;
Dumoutier L., Lejeune
Submitted (DEC-2000) |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kotenko S.V., Izotova L.S., Mirochnitchenko O.V Dickensheets H., Donnelly R.P., Pestka S.; "Identification, cloning, and characterization receptor that binds IL-22 and neutralizes its a J. Immunol. 166:7096-7103(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE=21286453;
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Wolk K., Asadullah K., Sabat
"A novel, soluble homologue c
preferential expression in pl
                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Godowski P.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      interPro;
                                                                                                                                                                                                                                                                                                                                                                                                 GO:0016020; C:membrane; IEA.
GO:0004896; F:hematopoietin/interferon-class (D200-domain.
GO:0004872; F:receptor activity; IEA.
erPro; IPR000282; Cytok receptor_2.
erPro; IPR008957; FN_III-like.
eptor; Signal.
98
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CDLTSB-TSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWETKIDPPVMNITQVNGSLLV
                                               CDVTDDITATV--PYNLRVRATLGSQTSAWSILKHPFNRNSTILTRPGMBITK-DGFHLV
                                                                                                                           PQNLSVLSTNMKHLLMWSPVIA-PGETVYYSVEYQGEYESLYTSHIWIPSSWCSLTEGPE
                                                                                                 PORVOFOSRNEHNILOWOPGRALTGNSSVYFVQYK----IYGQRQWKNKEDCWGTQELS
                                                                                                                                                                                                                                                                                                     231
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2:329-334(2001).
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231
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the EMBL/GenBank/DDBJ
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                                                                                                                                                                                                  Score 164.5; DB Pred. No. 2.7e-07 0; Mismatches 9
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                                                                                                                                                                                                                                                                                                                          soluble cytokine class isoform.
                                                                                                                                                                                                                                                                                                                                                                               Potential.
                                                                                                                                                                                                                                                                                                     24A6912BFF75100F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.V.,
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CARBOHYD
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Spencer S.D., Di Marco F., Hooley J., Pitts-Meek S., Spencer S.D., Di Marco F., Hooley J., Pitts-Meek S., Ryan A.M., Sordat B., Gibbs V.C., Aguet M.;
"The orphan receptor CRF2-4 is an essential subunit of the orphan receptor CRF2-4 is an essential subunit of 10 receptor.";
J. Exp. Med. 187:571-578(1998).
-i- FUNCTION: Receptor for IL10 and IL22. Serves as an expensive for the function of the following for the function of the following for the function of t
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                                                                                                                                                                                                                                         Glycoprotein;
SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=97199375; PubMed=90
Gibbs V.C., Pennica D.;
"CRF2-4: isolation of cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modified
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25-OCT-2004 (Rel. 45, Last annotation update)
Interleukin-10 receptor beta chain precursor (II
(Cytokine receptor family 2 member 4) (Cytokine
                                                                                                                                                                                                                                                                                         PROSITE; PS50853; FN3;
                                                                                                                                                                                                                                                                                                         InterPro; IPR000282; Cytok
InterPro; IPR008957; FN III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=IllOrb;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     L6-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          s SWISS-PROT entry is copyright. It is produced through a cween the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrict by non-profit institutions as long as its content is ified and this statement is not removed. Usage by and foities requires a license agreement (See http://www.isb-sib.send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Type I membrane protein. SIMILARITY: Belongs to the type II cytokine family c SIMILARITY: Contains 2 fibronectin type III domains.
                                                                                                                                                                                                                                                                                                                                                                    GO:0004920;
GO:0005515;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: Receptor for IL10 and IL22. Se essential for the active IL10 receptor c IL10-induced signal transduction events.
                                                                                                                                                                                                                                                                                                                                                                                                                  MGI:109380; Illorb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          186:97-101(1997).
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                                                                                                                                                                                                                                                                                                                                                               F:protein
                                                                                                                                                                                                                                                                                                                                                                                               F:interleukin-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=9047351; DOI=10.1016/S0378-1119(96)00690-7;
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Rodentia;
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Interleukin-10 recepto Extracellular (Potential Potential).

Cytoplasmic (Potential Fibronectin type-III 1 Fibronectin type-III 2 By similarity.

N-linked (GlcNAc. . .)
                                                                                                                                                                                                                                         Potential
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Murinae; Mus
        (Potential)
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OCT-2002 (TrEMBLrel. 20, Created)

O1-OCT-2003 (TrEMBLrel. 25, Last sequence upda

Interleukin 10 receptor 2 precursor.

Name=IllOrb; Synonyms=IllOr2;

Mus musculus (Mouse).

Eukaryota; Metazoo
                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                          Query Match
Best Local
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Best Local
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SEQUENCE
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                            Hardy M.P., Hertzog P.J., Ow
Submitted (OCT-2001) to the
EMBL, AF440787; AAL40946.1;
                                                                                                                                                                                                                                                                                                                                    Receptor; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                        PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=C57BL/6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                               ; MGI:109380; Ill0rb.
GO:0004920; F:interleukin-10 receptor
GO:0005515; F:protein binding; IPI.
RT; SM00060; FN3; 2.
SITE; PS50853; FN3; 1.
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                                                                                                                                                                                                                                                          Similarity
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 PGAAYCVKAQTFVKAIGRYSAFSQTECVEVQGEAI
                                               SLHLRFSAPQIENEPETWTLKNIYDSWAYRVQYWKN--GTNEKFQVVSPYDSEV-LRNLE
                                                                                  GFHL----VIE
                                                                                                                                                                         GMIPPPEKVRMNSVNFKNILQWEVPAFPKTNLTFTAQYE-SYRS-FQDH-----CKR
                                                                                                                                                                                                        VAILPAPQNLSVLSTNMKHLLMWSPVIAPGETVYYSVEYQGEYESLYTSHIWIPSSWCSL
                                                                                                            TASTOCOFS-HLSKYGDYTVRVRAELADEHSEWVNVTFCPV--EDTIIGPPEMQIESLAE
                                                                                                                                           TEGPECDVTDDITATVPYNLRVRATLGSQTSAW-SILKHPFNRNSTILTRPGMEITK--D
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ilarity 24.7%;
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24.7%;
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he EMBL/GenBank/DDBJ
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Pred. No. 1.2e
0; Mismatches
                                                                                                                                                                                                                                        Score 160; DB 2;
Pred. No. 1.2e-06;
0; Mismatches 92
                                                                                                                                                                                                                                                                                                     Potential.
: 53102D95809AF5D0 CRC64;
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N-linked (GlcNAc. . .) (P
N-linked (GlcNAc. . .) (P
; 58BA4F6B86330A39 CRC64;
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Sciurognathi; Muridae;
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; Murinae; Mus.
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ID I10S_HUMAN
AC Q08334;
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 Z17227;
U08988;
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01-FEB-1995
25-JAN-2005
                                                                                                                                                                                                                             interferon receptor-related proteins CRF2-4 and IL-22R."
J Biol. Chem. 275:31335-31339 (2000).
I- FUNCTION: Receptor for IL10 and IL22. Serves as an a essential for the active IL10 receptor complex and to IL10-induced signal transduction events.
IL10-induced signal transduction events.
ISUBCELLULAR LOCATION: Type I membrane protein.
ISIMILARITY: Belongs to the type II cytokine family one in the supplementation of the supplementation.
ISIMILARITY: Contains 2 fibronectin type III domains.
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"Structure of the human
                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20469498; PubMed=10875937; DOI=10.1074/jbc.M005304200; Xie M.-H., Aggarwal S., Ho W.-H., Foster J., Zhang Z., Stinson Wood W.I., Goddard A.D., Gurney A.L.; "Interleukin (IL)-22, a novel human cytokine that signals throu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 20-34.

PubMed=15340161; DOI=10.1110/ps.04682504;
Zhang Z., Henzel W.J.;

"Signal peptide prediction based on analyverified cleavage sites.";

Protein Sci. 13:2819-2824(2004).
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MEDLINE=93300510; PubMed=8314576;
MEDLINE=93300510; PubMed=8314576;
Lutfalla G., Gardiner K., Uze G.;
"A new member of the cytokine receptor
21 at less than 35 kb from IFNAR.";
Genomics 16:366-373(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97459974; PubMed=9312047; DOI=10.1093/emboj/16.19.
Kotenko S.V., Krause C.D., Izotova L.S., Pollack B.P., Wu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=96054036; PubMed=7563119;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Identification and functional characterization
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                                                          requires a license agreement (See http://www.isb-sib.
an email to license@isb-sib.ch).
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(Rel. 31, Last sequence update)
(Rel. 46, Last annotation update)
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CAA78933.1;
AAA86872.1;
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4) (Cytokine
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comparison with its
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Best Local S
Matches 57
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GO; GO:0005886; C:plasma membrane; TAS.
GO; GO:0004920; F:interleukin-10 receptor activity; TAS.
GO; GO:0004872; F:receptor activity; TAS.
GO; GO:0006955; P:immune response; TAS.
GO; GO:0006954; P:inflammatory response; TAS.
GO; GO:0006954; P:inflammatory response; TAS.
GO; GO:0007165; P:signal transduction; TAS.
InterPro; IPR000282; Cytok receptor_2.
InterPro; IPR000282; FN_III-like.
InterPro; IPR000187; FN_III-like.
INTERPRO; IPR00
                                                                                                                                                                                                                                                              Q9BUU4;
01-JUN-2001
01-JUN-2001
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CONFLICT
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                                                                                                                                   Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
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Name=IL10RB;
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                           SEQUENCE FROM
TISSUE-Kidney;
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HSSP; P13726;
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                                                      FROM N.A.
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1 (TrEMBLrel. 17, Last
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Glycoprotein; Receptor;
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Pred. No. 1.2e-06;
7; Mismatches 87
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Catarrhini; Hominidae;
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(GlcNAc. . .)
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                                                                                                                                   Buteleostomi;
; Homo.
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Submittedd (AUG-2003) to the EME
EMBL; BC001903; AAH01903.1; -.
EMBL; AY323826; AAP72016.1; -.
EMBL; BT009777; AAP88779.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Abramson R.D., Mullahy S.J., Rosak S.A., McEwan P.J., McKernan K.J., Abramson R.D., Mullahy S.J., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S. Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S. Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.E., Jones S.J., Marra M.A.; Skalska U., Smailus D.B., Schnerch A., Schein J.E., "Generation and initial analysis of more than 15,000 full-length human and mouse cNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF01108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro, IPR000282; Cytok ecept
InterPro, IPR003961; FN III-
InterPro, IPR008957; FN III-11ke.
InterPro, IPR001187; Tiësue facto
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Ahearn M.O., Kuldanek
Nickerson D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
Submitted (JAN-2001)
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GO:0016021; C:integral to membrane; IEA.
GO:0004896; F:hematopoietin/interferon-class
GO:0004872; F:receptor activity; IEA.
GO:0007596; P:blood coagulation; IEA.
                                             163
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                          LETMEPGAAYCVKAQTFVKAIGRYSAFSQTECVE-VQGBAIP
                                                                                                   DSLH---
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LRNLEPWITYCVQVRGFLPDRNKAGEWSEPVCEQTTHDETVP
                                                                                                                                                                                                    NTTLTECDFS-SLSKYGDHTLRVRAEFADEHSDWVNITFCPV--DDTIIGPPGMQVEVLA
                                                                                                                                                                                                                                                     LTEGPECDVTDDITATVPYNLRVRATLGSQTSAW-SILKHPFNRNSTILTRPGM--BITK 118
                                                                                                                                              DGFHLVIBLEDLGPOFE-----
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Kuldanek S
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                                                                                           -MRFLAPKIENEYETWTMKNVYNSWTYNVQYWKN--GTDEKFQITPQYDFEV-
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.A., Rajkumar N.,
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Pred. No. 1.2e
37; Mismatches
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h E.J., Yi Q.,
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ID Q6395
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Kacariyama S., Satoh N., Matsunawa H., Takahashi E., Kataoka R.,
Kuga N., Kuroda A., Satoh I., Kamata K., Takahashi E., Tarashima Y.,
Ka Watanabe M., Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A.,
Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M.,
Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Kanehori K.,
Kakikuchi H., Kanda K., Wagatsuma M., Murakawa K., Kanehori K.,
Xa Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.,
Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.,
Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.,
Sugano S., Nagahari K., Masuho Y., Nagai K., Jacogai T.,
Sugano S., Nagahari K., Masuho Y., Nagai K., Jacogai T.,
Sugano S., Nagahari K., Masuho Y., Nagai K., Jacogai T.,
Sugano S., Nagahari K., Masuho Y., Nagai K., Jacogai T.,
Sugano S., Nagahari K., Masuho Y., Nagai K., Jacogai T.,
Sugano S., Nagahari K., Masuho Y., Nagai K., Jacogai T.,
Sugano S., Nagahari K.,
Sugano S., Nagahari K., Jacogai T.,
Sugano S., Nagahari K.,
Sugano S., Nagahari K.,
Sugano S., Nagahari K., Jacogai T.,
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Q6ZVU9;
05-JUL-2004
05-JUL-2004
05-JUL-2004
Name=Ifngr2; Synonyms=ifngr2;
Mus musculus (Mouse).
Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI TaxID=10090;
[1]
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SEQUENCE
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TISSUE-Synovial membrane tissue;
Suzuki O., Sasaki N., Aotsuka S., Shoji T., Ichihara T.,
Suzuki O., Sasaki N., Sano S., Nomura R., Yoshikawa Y.
Matsumoto K., Hirano M., Sano S., Momivama H., Onogawa S
                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel. 01, Creat
01-NOV-1996 (TrEMBLrel. 01, Last
25-OCT-2004 (TrEMBLrel. 28, Last
Ifngr2 protein (Interferon gamma
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57; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DSLH----MRFLAPKIENEYETWTMKNVYNSWTYNVQYWKN--GTDEKFQITPQYDFEV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 327 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37430 MW; DACB38F7312B0EF6 CRC64;
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Pred. No. 1.
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es 87; Indels 41;
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Best Local &
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EMBL; U6594; AACS2938.1; JOINED.
EMBL; U69596; AACS2938.1; JOINED.
EMBL; U69595; AACS2938.1; JOINED.
EMBL; U69595; AACS2938.1; JOINED.
EMBL; U69598; AACS2938.1; JOINED.
EMBL; U69598; AACS2938.1; JOINED.
EMBL; U69598; AACS2938.1; JOINED.
EMBL; BC055745; AAM55745.1; -.
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Submitted
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STRAIN=129Sv/J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00041; fn3; 1.
SMART; SM00060; FN3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=C57BL/6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and mouse cDNA sequences."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0005615; C:extracellular space; 7
GO; GO:0016021; C:integral to membrane;
InterPro; IPR000282; Cytok receptor_2.
InterPro; IPR003961; FN_III.
InterPro; IPR008957; FN_III-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50853; FN3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Generation and initial analysis of more
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MGI:107654; Ifngr2.
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                                                                ILTRP--GMEITKDGFHLVIELE---DL--GPQFEFLVAYWRREPGABEHVK-MVRSGGI
                                                                                                                                     RLLE-PNCTDITETKCDLTGGGRLKLFPHPFTVFLRVRAKRGNLTSKWVGLE-PFQHYEN
                                                                                                                                                                                              SLTEGPEC-DVTD---DITA-----TVPYN--LRVRATLGSQTSAWSILKHPFNRNST
                                                                                                                                                                                                                                                                                          DSFSQLAAPLNPRLHLYNDEQILTWEP--SPSSNDPRPVVYQVEYS----FIDGSWH
                                                                                                                                                                                                                                                                                                                                                              DEVAILPAPONLSVLSTNMKHLLMWSPVIAPGETVYYSVEYOGEYESLYTSHIWIPSSWC
VTVGPPKNISVTPGKGSLVIHFSPPFDVFHGATFQYLVHYWEKSETQQEQVEGPFKSNSI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        332 AA; 37471 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Brain;
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hee S., Muthukumaran G., Lembo D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sci. U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               29;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 158; DB 2;
Pred. No. 1.7e-06;
9; Mismatches 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99:16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E2DD53BF934BA087 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           than 15,000
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160

PVHLETMEPGAAYCVKAQTFV----KAIGRYSAFSQTECVEVQGEA

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RESULT 14
QGUMM1
ID QGUMA
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Best Local :
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05-JUL-2004
05-JUL-2004
05-JUL-2004
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SEQUENCE
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MEDLINB=94170381; PubMed=8124717; DOI=10.10

Hemmi S., Bohni R., Stark G., Di Marco P.,

"A novel member of the interferon receptor
functionality of the murine interferon gamm
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05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
                                                                      Bukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000282; Cytok_receptor_2.
InterPro; IPR009391; FN_III.
InterPro; IPR008957; FN_III-11ke.
Pfam; PF00041; fn3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                        NCBI_TaxID=9606;
                                                                                                                      Homo sapiens (Human)
                                                                                                                                             ORFNames=UNQ5793;
                                                                                                                                                                         IL22RA2.
                                                                                                                                                                                                                                                                                             Q6UWM1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cell 76:803-810(1994).
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Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q78EC1;
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GO:0004896; F:hematopoietin/interferon-class
GO:0004872; F:receptor activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                    193
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                                                                                                                                                                                                                                                                                                                                                                                                               V--LGNLKPYRVYCLQTEAQLILKNKKIRPHGLLSNVSCHETTANA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            PVHLETMEPGAAYCVKAQTFV----KAIGRYSAFSQTECVEVQGEA
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                                                                                                                                                                                             (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            332 AA;
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                                                                                                                                                                                                                                                                                             PRELIMINARY,
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MBLrel. 27, Last sequen
MBLrel. 27, Last annota
receptor beta subunit.
                                                                      Chordata;
Primates;
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                                                                                                                                                                                             27,
27,
27,
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                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                             Last sequence update)
Last annotation update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 158; DB 2;
Pred. No. 1.7e-06;
9; Mismatches 94
                                                                      Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E2DD53BF934BA087 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOI=10.1016/0092-8674(94)90355-7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 332;
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RESULT 15
Q969J5
                       REPRESENTATION OF THE PROPERTY                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
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Best Local Similarity
Matches 59; Conserv
MBDLING.
KOtenko S.V., Izocore
Dickensheets H., Donne
"Identification, clone
"Identification that binds I
                                                                                                                                                                                                                                              TISSUE=Placenta; PubMed=11607789; DOI=10.1038/sj.gene.6363786; MEDLINB=21518574; PubMed=11607789; DOI=10.1038/sj.gene.6363786; Gruenberg B.H., Schoenemeyer A., Weiss B., Toschi L., Kunz S., Wolk K., Asadullah K., Sabat R.; "A novel, soluble homologue of the human II-10 receptor with preferential expression in placenta."; Genes Immun. 2:329-334(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Soluble cytokine class II receptor, long isoform pro
(Interleukin 22-binding protein CRF2-10L)
Name=CRF2-S1; Synonyms=IL22BP;
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003; Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J. Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd Baton D., Foster J., Grimaldi C., Gu Q., Hass P.B., Heldens S., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Seshagiri S., Simons L., Singh J., Smith V., Stinson J., Vagts A Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I., Cherki P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q969J5
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GO; GO:0004896; F:hematopoletin/interferon-class
InterPro; IPR000282; Cytok_receptor_2.
InterPro; IPR008957; FN III-like.
SEQUENCE 262 AA; 30418 MW; E46EEF4DE78ADFDA C
                                                                                                                                                                        MBDLINE=21286453; PubMed=11390454;
                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
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HSSP; P24055; 1A21.
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Genome Res. 13:2265-2270(2003).
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               Izotova L.S., Mirochnitchenko O.V., H., Donnelly R.P., Pestka S., on cloning, and characterization of binds IL-22 and neutralizes its activation of the control of the cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Primates;
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25.0%;
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Pred. No. 5.
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                   n of a novel activity.";
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Search completed: February 25, 2005, 02:43:36 Job time : 109.724 secs
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                                                                                                                                                                                                                                                               Query Match 14.0%; Score 151.5; DB 2; Length 263; Best Local Similarity 25.0%; Pred. No. 5.3e-06; Matches 59; Conservative 32; Mismatches 94; Indels 51; Gaps
                                                                                                                                                                                                                                                                                                                                                                                   J. Immunol. 166:7096-7103(2001).

EMBL; AJ313162; CAC85635.1; -.

EMBL; AV040567; AAC85715.1; -.

HSSP; P24055; 1A21.

Go; GO:0016020; C:membrane; IEA.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0004895; F:hematopoietin/interferon-class (D200-domain. GO; GO:0004872; F:receptor activity; IEA.

InterPro; IPR000282; Cytok_receptor_2.

InterPro; IPR000282; Cytok_receptor_2.
                                                                                                                                                                                                                                                                                                                                               Receptor; Signal.
SIGNAL 1
CHAIN 22
                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                 KHPFNRNSTILTRPGMEITK-DGFHLVI------ELEDLGPQFEFLVAYW 141
                                                                                                                                                                                     1 21 Potential.
22 263 soluble cytokine class II receptor, long
isoform.
263 AA; 30550 MW; C96BCBC5D78AC79B CRC64;
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Result
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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: uniprot_sprot:*
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Gapop 10.0 , Gapext 0.5
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1 VPCVSGGLPKPANITFLSIN......PSEKQCARTLKDQSSEFKAK 221
     1612378 seqs, 512079187 residues
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Copyright (c) 1993 - 2005 Compugen Ltd
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Q9uhf4 homo sapien
Q6pbb0 mus musculu
Q95sh7 homo sapien
Q96a41 homo sapien
Q96a41 homo sapien
Q96a41 homo sapien
Q80091 tetracdon n
Q7tn14 rattus norv
Q6uwml homo sapien
Q7tn15 mus musculu
Q80xf5 mus musculu
Q80xf5 mus musculu
Q9ygc8 gallus gall
Q6zvu9 homo sapien
Q7tn17 sus scrofa
Q80081 tetracdon n
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Q80084 tetracdon n
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Q80086 tetracdon n
Q80088 musculu
Q7400 gallus gall
Q9yhw0 gallus gall
Q9yhw0 gallus gall
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Q8n6p7 homo sapien
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		AA.	553	PRT;	•	STANDARD;	S	AN R_HUMAN	RESULT 1 120R_HUMAN ID 120R_HUMAN
		-	AL I GNMENTS	ALI					
oncorhynchu	Q90w13			Q90W13	N		13.3	159.5	45
homo sapien	Q9by69			Q9BY69	N		13.5	161.5	44
cavia porce	Q9jlu8		S	TF_CAVPO	ш		13.5	162	43
homo sapien	P15260		MAN	INGR_HUMAN	-		13.6	163.5	42
ovis aries	Q28589		HEBP	INR1_SHEEP	μ.	560	13.9	166.5	41
homo sapien	Q8wtz2			Q8WTZ2	N		13.9	166.5	40
homo sapien	Q6pkd7			Q6PKD7	N		13.9	166.5	39
ovis aries	Q9gk86			Q9GK86	N		13.9	166.5	38
tetraodon n	Q7zt35			Q7ZT35	N		14.0	167.5	37
homo sapien	P17181		UMAN	INR1_HUMAN	_		14.0	168.5	36
tetraodon n	Q7zt22			Q7ZT22	N		14.8	177.5	35
mus musculu	Q80xz4			Q80XZ4	N		15.2	183	34
bos taurus	Q04790		OVIN	INR1_BOVIN	ш		15.5	186.5	33
sus scrofa	Q764m8		-	Q764M8	N		15.6	187	32

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Burford D.C., Burfill W., Burton J., Carder C., Carter N.P., Collier R.E., Collins J.E., Colman L.K., Corby N.R., Coville G.J., Culley K.M., Dhami P., Davies J., Dunn M., Earthrowl M.E., Ellington A.E., Evans K.A., Faulkner L., Francis M.D., Frankish A., Frankland J., French L., Garner P., Garnett J., Ghori M.J., Gilby L.M., Gillson C.J., Glithero R.J., Grafham D.V., Grant M.,	a J.P., Ambrose K.D., Andrews T.D., Ashwell R.I.S. e A.K., Bagguley C.L., Bailey J., Banerjee R., Bas K.F., Bates K., Beare D.M., Beasley H., Beasley G., S. R. Brown A.J. Brown	SEQUENCE FROM N.A. MEDLINE-22935763; PubMed=14574404; DOI=10.1038/nature02055; Mungall A.J., Palmer S.A., Sims S.K., Edwards C.A., Ashurst J.L., Wilming L., Jones M.C., Horton R., Hunt S.B., Scott C.B., Gilbert J.G.R., Clamp M.B., Bethel G., Milne S., Ainscough R.,	ലവരമ	Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A., Vandlen R., Watanabe C., Wieand D., Woods K., Xie MH., Yansura D., Yi-S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I., Godowski P., Gray A.;	NCE FROM N.A. (ISOFORM 2). NB=22887296; PubMed=12975309 H.F., Gurney A.L., Abaya E. J., Chow B., Chui C., Crowle D., Foster J., Grimaldi C., A. Kim H.S., Klimowski L.	SEQUENCE FROM N.A. (ISOFORM 1). SEQUENCE FROM N.A. (ISOFORM 1). Lok S., Kho C., Jelmberg A., Adams R., Whitmore T., Farrah T., O'Hara P.; "Homo sapiens cytokine receptor homolog."; Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.	Name=ILioRa; Synonyms=ZCYTOR7; Name=ILioRa; Synonyms=ZCYTOR7; Homo sapiens (Human). Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;	_ 1 • 2

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RA Holmes S.J., Howden P.J., Howe K.I., Howell G.R., Huckle E.,
RA Humphray S.J., Howden B.J., Howe K.I., Howell G.R., Huckle E.,
RA Humphray S.J., Kimberley A.M., King A., Laird G.K., Langford C.,
RA Kay M., Keenan S.J., Kimberley A.M., King A., Laird G.K., Langford C.,
RA Lawlor S., Leongamornlert D.A., Leversha M., Lloyd C.R., Lloyd D.M.,
RA Lawlor S., Leongamornlert D.A., Leversha M., Lloyd C.R., Lloyd D.M.,
RA Lawlor S., Leongamornlert D.A., Leversha M., Lloyd C.R., Lloyd D.M.,
RA Lawlor S., Leongamornlert D.A., Eversha M., Lioyd C.R., Lloyd D.M.,
RA Maslen G.L., Matthews L., McCann O.T., McLaren S.J., McLay K.,
RA McMurray A., Moore M.J.F., Mullikin J.C., Niblett D., Nickerson T.,
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RA Nowik K.L., Oliver K., Overton-Larty E.K., Parker A., Patel R.,
RA Porter K.M., Ramsey Y., Ranby S.A., Rice C.M., Ross M.T., Searle S.M.,
RA Schra H.K., Sheridan E., Skuce C.D., Smith S., Smith M., Spraggon L.,
RA Squares S.L., Steward C.A., Sycamore N., Tamlyn-Hall G., Tester J.,
RA Theaker A.J., Thomas D.W., Thorpe A., Tromans A., Tubby B.,
RA Whittaker H., Wild A., West A.P., White S.S., Whitehead S.L.,
RA Wyatt J.C., Young L., Younger R.M., Bentley D.R., Coulson A.,
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Anantha S., Dickensheets
Donnelly R.P., Kotenko S.
"IL-26 signals through a
receptor 1 and IL-10 rece
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complexes. Diff biological func J. Biol. Chem.
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MEDLINE-21097717; PubMed=11163236; DDI=10.1016/S0092-8674(01)00187-8;
Blumberg H., Conklin D., Xu W.F., Grossmann A., Brender T.,
Carollo S., Eagan M., Foster D., Haldeman B.A., Hammond A., Haugen H.,
Jelinek L., Kelly J.D., Madden K., Maurer M.F., Parrish-Novak J.,
Prunkard D., Sexson S., Sprecher C., Waggie K., West J.,
Whitmore T.E., Yao L., Kuechle M.K., Dale B.A., Chandrasekher Y.A.;
"Interleukin 20; discovery, receptor identification, and role in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gribble
Hammond
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PubMed=12351624; DOI=10.1074/jbc.M205114200;

Parrish-Novak J., Xu W., Brender T., Yao L., Jones C., W
Brandt C., Jelinek L., Madden K., McKernan P.A., Foster
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"Interleukins 19, 20, and 24 signal through two distinct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=15340161; DOI=10.1110/ps.04682504; Zhang Z., Henzel W.J.; "Signal peptide prediction based on analy
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Cell 104:9-19(2001).
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                                                                                                                                                                                           SUBUNIT,
                                                                                                                                                                                                                                                     Biochemistry
                                                                                                                                                                                                                                                                                      "Characterization of the recombinant extracellular domains of human interleukin-20 receptors and their complexes with interleukin-19 and interleukin-20.";
                                                                                                                                                                                                                                                                                                                                                                                Wlodawer A., Zdanov A.;
                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=14580208; DOI=10.1021/bi0354583;
Pletner S., Magracheva E., Kozlov S., Tobin
                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=14580208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT, AND LIGAND BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=11564763;
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S., Harley J.L., Hart E.A., Heath P.
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                                Dickensheets H., Du
P., Kotenko S.V.;
als through a novel
                                                                                                                                                                                                                                                  42:12617-12624(2003).
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                                                                                                                          Lewis-Antes
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Heath P.D., Heathcott
Howell G.R., Huckle F
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L., Renauld
                                   complex composed of IL-20
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interactions mediate un;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            experimentally
                                                                                       Smirnov S.V., J.C., Zdanov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Halls K.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       West J
r D.C.,
                                                                                                                                                                                                                                                                                                                                                                                                          S.V.,
                                                                                             Zdanov A.,
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-!- FUNCTION: The IL20RA/IL20RB dimer is a receptor for IL19, IL20R. The IL20RA/IL10RB dimer is a receptor for IL26.
-!- SUBUNIT: Heterodimer with IL20RB and heterodimer with IL10RB SUBCELLULAR LOCATION: Type I membrane protein (By similar:
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                          MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF184971; AAF01320.1;
EMBL; AY358883; AAQ89242.1;
EMBL; AL135902; CAC38375.1;
HSSP; P13726; 2HFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as modified and this statement is not removed. It entities requires a license agreement (See httors end an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This
                                                                                      SEQUENCE
                                                                                                                                           VARSPLIC
                                                                                                                                                                VARSPLIC
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                                                                                                                                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                                                                                 Receptor;
                                                                                                                                                                                                                                                                                                                                                            Alternative
                                                                                                                                                                                                                                                                                                                                                                     PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        between
                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
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                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    skin. SIMILARITY: Belongs to the type II cytokine family of SIMILARITY: Contains 2 fibronectin type III domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and testis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                          605620;
                                            221;
                                                                                                                                                                                                                                                                                                                                                                                 PF01108;
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SSUE SPECIFICITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IsoId=Q9UHF4-1; Sequence=Displayed,
                                                                                                                                                                                                                                                                                                                                                                                                                                   HGNC:6003; IL20RA.
                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                        01108; Tissue_fac; I.
PS50853; FN3; FALSE_NEG.
ive_splicing; Direct_protein sequencing; Glycoprotein;
              VPCVSGGLPKPANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYFIYGQKKWLNKSECRN
UPCVSGGLPKPANITELSINMKNVLQWTPPEGLQGVKVTYTVQYFIYGQKKWLNKSSCRN
                                                                                                                                                                                                                                                                                                                                                                                        IPR000282; Cytok_receptor_2.
IPR008957; FN_III-like.
IPR001187; Tissue_factor.
                                                                                                                                                                                                                                                                                                                                                 Repeat;
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nilarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence=VSP_011497, VSP_011498;
Y: Widely expressed with highest levels
gh levels in brain. Highly expressd in p
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Fibronectin (
Fibronectin (
                                                                                                                    /FTId=VSP_011497.
VKAIWGTKCSKWAESGRFYPFLET
LKLLTLCSISS (in isoform ;
/FTId=VSP_011498.
                                                                                                                                                                                                                                                              Poly-Glu
                                                                                                                                                                                                                                                                                                                  Interleukin-20 receptor alpha
Extracellular (Potential).
                                           Score 1200; DB 1;
Pred. No. 7.9e-100;
; Mismatches 0;
                                                                                       7C23C8543B114659
                                                                                                  r <
                                                                                                VSP_011498.
(in Ref. 2
(in Ref. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                       type-III
                                                                                                                                                                                                                                                                                              (Potential).
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RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Nikaido I., Osato N., Baito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Schriml L.M., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Glasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Kanai A., Kawaji H., Marchionni L., McKenzie L., Miki H.,
RA Naggahima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Nagsahima T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Milming E., Mayashizaki Y.,
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25-OCT-2004 (Re]
25-OCT-2004 (Re]
25-OCT-2004 (Re]
STRAIN=129; TISSUE=Breast tumor;

MEDLINE=22388257; PubMedc12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Walek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Analysis of the mouse transcriptome 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=129; TISSUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-C57BL/60; TISSUE-Oviduct;
MEDLINE-22354683; PubMed-12466851; DOI-10.1038/nature01266;
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Mammalia; Eutheria;
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(Rel. 45, Last sequence update)
(Rel. 45, Last annotation update)
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EMBL; BC056628; AAH56628.1; -.
HSSP; P13726; ZHFT
InterPro; IPR000282; Cytok receptor_2.
InterPro; IPR008957; FN III-like.
InterPro; IPR001187; Tissue_fac; I.
Pfam; PF01108; Tissue_fac; I.
PROSITE; PS50853; FN3; FALSE_NEG.
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DISULFID
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CARBOHYD
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CHAIN 3
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TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fahey J., Helton E., Ketteman M., Madan A., Rodrigu Whiting M., Madan A., Young A.C., Shevchenko Y., Boy Blakesley R.W., Touchman J.W., Green E.D., Dickson! Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M. Butterfield Y.S.N., Krzywinski M.I., Skalska U., Sm Schnerch A., Schein J.B., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,00
                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                y Match
Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              similarity).
SUBCELLULAR LOCATION:
SIMILARITY: Belongs to
SIMILARITY: Contains 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 similarity)
SUBUNIT: He
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002). FUNCTION: The IL20RA/IL20RB dimer is a receptor IL24. The IL20RA/IL10RB dimer is a receptor for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mouse cDNA sequences.";
                                                       121
                                                                                                                                                                                      176;
                                                                                  93
                                                                                                          61
                                                                                                                                   3
                                                                                                                                                                                                  Similarity
   PNTLYCVHVESFVPGPPRRAQPSEKQCARTLKDQSSEFKAK
                                              SISVVLTAPEK#KRNPEDLPVSMQQIYSNLKYNVSVLNTKSNRT#SQCVTNHTLVLT#LE
                                                                                              INRTYCDLSAETSDYBHQYYAKVKAIWGTKCSKWAESGRFYPFLETQIGPPEVALTTDEK
                                                                                                                                                  VPCVSGGLPKPANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYPIYGQKKWLNKSECRN
                                 SISIALTAPEKWKRNPQDHT
                                                                                 INRTYCOLSVETSDYEHQFYAKVKAIWEARCSEWAETERFYPFLETQVSPPEVALTTGEK
                                                                                                                                   VPCVFCGLPKPTNITFLSINMKNVLHWNPPESLHGVEVTYTVQYFIYGQKKWLNASKCGS
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                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: Type I membrane protein (By 81 Belongs to the type II cytokine family o Contains 2 fibronectin type III domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E., Ketteman M., Madan A., Rodrigues
n A., Young A.C., Shevchenko Y., Bouff
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79.6%;
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Potential
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                                                                                                                                                                                      15;
                                                                                                                                                                                                                                               Potential.

Cytoplasmic (Potential Cytoplasmic (Potential Fibronectin type-III 1 Fibronectin type-III 2 Pibronectin type-III 2 By similarity.

By similarity.

N-linked (GlcNAc...)

                                                                                                                                                                                Score 965; DB
Pred. No. 1.4e
15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                         Interleukin-20 receptor a 
Extracellular (Potential)
                                                                                                                                                                                                                                       E7EC07DA2D49AF7F
                                                                                                                                                                                                                                                                                                                                                                                                                                               Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Transmembrane
                                                                                                                                                                                                4e-78
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                                                                                                                                                                                                                                                                                                                                                                                 (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  heterodimer with IL10RB
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1 G.G.,
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Best Local S
Matches 171
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01-DEC-2001
01-OCT-2003
TISSUE=Mammary gland;
MEDLINE=21518574; PubMed=11607789; DOI=10.1038/sj.
Gruenberg B.H., Schoenemeyer A., Weiss B., Toschi
Wolk K., Asadullah K., Sabat R.;
"A novel, soluble homologue of the human IL-10 rec
"referential expression in placenta.";
Genes Immun. 2:329-334(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Receptor.
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q96A41;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Soluble cytokine class II receptor, short isoform precursor
(Interleukin 22-binding protein CRF2-10) (Class II cytokine
(IL2ZRA2).
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Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. Griffiths C.;
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                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=CRF2-S1; Synonyms=IL-22BP,
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GO:0004896; F:hematopoietin/interferon-class
GO:0004872; F:receptor activity; IEA.
erPro; IPR000282; Cytok receptor 2.
erPro; IPR008957; FN_III-like.
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P13726; 2HFT.
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(TrEMBLrel. 19,
(TrEMBLrel. 25,
(Interleukin 20
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                                                                                                                                                                                                                                                                                                                                                                                                                             (Human)
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Primates;
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90.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Ve
Catarrhini;
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                                                                                                                                                        .gene.6363786;
L., Kunz S.,
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Genome Res. 13:2265-2270(2003).
EMBL; AJ313161; CAC85634.1; -.
EMBL; AJ297262; CAC83097.1; -.
EMBL; AY204565; AAK85714.1; -.
EMBL; AY004565; AAK857175.1; -.
EMBL; AY358111; AAQ88478.1; -.
HSSP; P24055; IAZ1.
CC. COLOROSOS, IAZI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21396522; PubMed=11481447; DOI=10.1073/pnas.171303198; Xu W. Presnell S.R., Parrish-Novak J., Kindsvogel W., Jaspers S., Chen Z., Dillon S.R., Gao Z., Gilbert T., Madden K., Schlutsmeyer: Yao L., Whitmore T.E., Chandrasekher Y., Grant F.J., Maurer M., Jelinek L., Storey H., Brender T., Hammond A., Topouzis S., Clegg C.H., Foster D.C.; "A soluble class II cytokine receptor, IL-22RA2, is a naturally occurring IL-22 antagonist."; Proc. Natl. Acad. Sci. U.S.A. 98:9511-9516(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003; Clark H.F., Gurney A.L., Abaya B., Baker K., Baldwin D., Brush Chen J., Chow B., Chni C., Crowley C., Currell B., Deuel B., E Baton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S. Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld
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GO; GO:0004896; F:hematopoletin/interferon-class
GO; GO:0004872; F:receptor activity; IEA.
InterPro; IPR000282; Cytok receptor 2.
InterPro; IPR008957; FN_III-like.

DECENTRY (IPR008957); FN_III-like.
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Tetraodon nigroviridis (Green puffer).
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Tetradontoidea; Tetraodontidae; Tetraodon.
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Helical cytokine receptor CRFBB.
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BMC Genomics 4:29-29(2003).
EMBL; Au544894; CAD67782.1; -.
GO; GO:0016920; C:membrane; IEA.
GO; GO:0004896; F:hematopoietin/interferon-class
GO; GO:0004872; F:receptor activity; IEA.
InterPro; IPR000282; Cytok receptor 2.
InterPro; IPR008957; FN_III-like.
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Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <u>Α</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EPNTLYCVHVESFVPGPPRRAQPSEKQCARTLKD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63848 MW; A8A38DC3BF78ABE2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 333.5;
; Pred. No. 1.86
41; Mismatches
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                                                                          Percomorpha;
Tetraodon.
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                                                                                                                                          Vertebrata; Euteleostomi;
Euteleostei; Neoteleostei;
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                                                             HSSP; P13726; IJPS.
HSSP; P13726; IJPS.
GO; GO:0016020; C:membrane; IEA,
GO; GO:0004896; F:hematopoietin/interferon-class
GO; GO:0004897; F:receptor activity; IEA.
InterPro; IPR000282; Cytok receptor_2.
InterPro; IPR008957; FN_III-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q7TNI4;
01-OCT-2003 (
01-OCT-2003 (
01-MAR-2004 (
                    Receptor;
SIGNAL
CHAIN
                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q7TNI4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Comparative genomic analysis reveals independent expansion of lineage-specific gene family in vertebrates: The class II cytol receptors and their ligands in mammals and fish.";
  SEQUENCE
                                                                                                                                                                                                                    Genes Immun.
                                                                                                                                                                                                                                                                                            STRAIN=Sprague-Dawley; TISSU
Weiss B., Wolk K., Gruenberg
                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cytokine receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                         "Cloning of murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=crf2-s1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lutfalla G., Roest Crollius H., Mogensen K., Monneron D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      L; AJ544911; CAD67769.1; -.
GO:0016020; C:membrane; IEA.
GO:0004896; F:hematopoietin/interferon-class
GO:0004872; F:receptor activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genomics 4:29-29(2003).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118 DEKSISVVLTAPEKWKRNPEDLPVSMQQIYSNLKYNVSVLNTKSNRTWSQCVTNHTLVLT
                                                                                                                                                                                             Immun. 5:330-336(2004).
AJ555485; CAD88475.1; -
                                                                                                                                                                                                                                  counterpart."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLYKHHLABYNKEYCFSVKAKFLAMPVQCQSSEWQCITTPTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENSNAI VTVKGPMRYQPNFQMPAVSMATIYPHMMYNLSIRNTYRNK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VSASLPSPTSVFIASVNLRNVLEWTPGNDTPS-NATFTVQYAIYGDSDKRRSVRWRALQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VSGGLPKPANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYFIYGQK-----KWLNKSE
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                                                     Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR000282; Cytok_receptor_2.
IPR008957; FN_III-like.
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  229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. 25, (TrEMBLrel. 25, (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  568 AA; 63834 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel.
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                229
                                                                                                                                                                                                                                                       IL-22 receptor alpha
                                                                                                                                                                                                                                                                                                                                                                                               Chordata;
Rodentia;
  26721 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27.8%;
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                                                                                                                                                                                                                                                                                          TISSUE=Spleen;
enberg B.H., Vo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
soluble 1 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
cytokine receptor family 
5CFFD37652A99365 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                Volk
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                                                                                                                                     (D200-domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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Matches 74
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Best Local S
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                                                                                                                                                                                                  GO; GO:0016020; C:membrane; IEA.
GO; GO:0004896; F:hematopoletin/interferon-class
InterPro; IPR000282; Cytok_receptor_2.
InterPro; IPR008957; FN III-like.
SEQUENCE 262 AA; 30418 MW; E46EEF4DE78ADFDA C
                                                                                                                                                                                                                                                                  EMBL; AY358737; AAQ89097.1; HSSP; P24055; 1A21.
                                                                                                                                                                                                                                                                                                                    "The secreted protein discovery initiative effort to identify novel human secreted and
                                                                                                                                                                                                                                                                                                                                                     Vandlen R., Watanabe C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TWMD90
                                                                                                                                                                                                                                                                                          bioinformatics assessment.";
Genome Res. 13:2265-2270(2003).
                                                                                                                                                                                                                                                                                                                                                 Godowski P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                     KPANITELSINMKNVLQWTPPEGLQGVKVTYTVQYFI-----------
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                                       FPGCRTLAKYGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSMT
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                                                                                            KPQRVQFQSRNFHNILQWQPGRALTGNSSVYFVQYKIMFSCSMKSSHQKPSGCWQHISCN
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Primates;
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                                                                                                                                           Score 310; DB
Pred. No. 9e-20
33; Mismatches
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Last annotation updat
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Pred. No. 2.7e-20;
0; Mismatches 97
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No. 9e-20;
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A KOtenko S.V., Izotova I.S., Mirochnitchenko O.V., Esterova E.
A Dickensheets H., Donnelly R.P., Pestka S.;
A Dickensheets H., Donnelly R.P., Pestka S.;
I receptor that binds IL-22 and neutralizes its activity.";
I Immunol. 166:7096-7103 (2001).
I Immunol. 170: CAC85635.1; -.
R EMBL; AJ313162; CAC85635.1; -.
R EMBL; AV313162; TAZ1.
R EMBL; AV040567; AAX85715.1; -.
R HSSP; P24055; IAZ1.
R GG; GO:0016020; C:membrane; IEA.
R GG; GO:0014872; F:heematopoietin/interferon-class (D200-domain R GG; GO:0004872; F:hematopoietin/interferon-class (D200-domain R GG; GO:0004872; F:hematopoietin/interfer
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Best Local
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Q969J5;
01-DEC-2001
01-DEC-2001
05-JUL-2004
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Soluble cytokine class II receptor, long isoform pri
(Interleukin 22-binding protein CRF2-10L)
Name=CRF2-S1; Synonyms=IL22BP;
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "A novel, soluble homologue of the human preferential expression in placenta."; Genes Immun. 2:329-334(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Receptor; Signal.
SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gruenberg B.H., Schoen
Wolk K., Asadullah K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21518574; PubMed=11607789; DOI=10.1038/sj
Gruenberg B.H., Schoenemeyer A., Weiss B., Toschi
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM
MEDLINE=21286
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NNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERC
                                            NTKSNRTWSQCVTNHTLV-LTWLEPNTLYCVHVESFVPGPPRRAQPSEKQC
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lah K., Sabat
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Pred. No. 9.1e-20;
3; Mismatches 90
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L., Kunz S.,
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Best Local S
Matches 65
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Q7TNI5;
01-OCT-2003 (TrEMBI
01-OCT-2003 (TrEMBI
01-MAR-2004 (TrEMBB
01-MAR-2004 (TrEMBB
                                                                                                                                                                               Q80XF5
Q80XF5;
Q1-JUN-2003
01-JUN-2003
01-MAR-2004
                                                                                                                                           01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation updat
Interleukin 22 soluble receptor.
Name=Il22ra2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Receptor;
SIGNAL
SEQUENCE FROM N.A.
STRAIN-BALB/c;
MEDLINE=22586333; PubMed=12700595;
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EMBL;
HSSP;
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STRAIN-Balb/c; TISSUE-Spleen;
Weiss B., Wolk K., Gruenberg
                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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Mammalia; Eutheria;
                                                                                                                            Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=CRF2-s1;
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GO:0005515; F:protein binding; IPI.
GO:0042516; P:regulation of tyrosine
erPro; IPR000282; Cytok receptor_2.
erPro; IPR08957; FN_III-like.
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P13726; 1JPS
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65; Conserv
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                                                                                           Chordata;
Rodentia;
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230
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Rodentia;
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Pred. No. 7.4e-17;
0; Mismatches 99
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soluble 1.
page 4EDFBAFC105
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                                                                                       Craniata; Vertebrata; Sciurognathi; Muridae;
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Sciurognathi; Muridae;
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annotation update)
y II soluble 1 precursor.
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 DOI=10.1038/sj.gene.6363947;
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Murinae; Mus
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L Genome Res. 9:242-250(199).
R EMBL; AF082667; AAD13678.1; -.
R EMBL; AF082666; AAD13671.1; -.
R GO; GO:0016021; C:integral to membrane; IEA.
R GO; GO:0004896; F:hematopoietin/interferon-class (D: GO:0004872; F:receptor activity; IEA.
R GO; GO:0004872; F:receptor activity; IEA.
R GO; GO:0007596; F:blood coagulation; IEA.
R InterPro; IPR000282; Cytok receptor_2.
RINTERPO; IPR003961; FN_III_like.
RINTERPO; IPR003961; TiBsue_factor.
Pfam; PF01108.
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Best Local
Matches 6
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Name=IL10R2;
Name=IL10R2;
Gallus gallus (Chicken).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; C
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Q9YGC8;
01-MAY-1999
01-MAY-1999
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Receptor.
SEQUENCE
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Interleukin-10
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STRAIN=BALB/c;
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                                                                                                                                                                                                                                                                                                                            MEDLINE=99177346; PubMed=10077530;
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9031;
[1]
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GO:0005515; F:protein binding; IPI.
GO:0042516; P:regulation of tyrosine
GO:0042516; P:regulation of tyrosine
erPro; IPR000282; Cytok receptor 2.
erPro; IPR008957; FN_III-like.
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; P13726; LUPS.
MGI:2665114; I122ra2.
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llarity 31.7%;
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Tissue_fac;
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Pred. No. :
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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use IL-22 binding protein.";
                                                                                                                                                                                                                                                                                   Uze G., Lutfalla G.;
interferon/interleukin-10
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L.1e-16;
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맑 Ş 밁 Ś 밁

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W [1]

SEQUENCE FROM N.A.

RP SEQUENCE FROM N.A.

RP SEQUENCY STATESUBE-Synovial membrane tissue;

RC TISSUB-Synovial membrane tissue;

RA Suzuki O., Sasaki N., Aotsuka S., Shoji T., Ichihara T., Suzuki O., Sasaki N., Aotsuka S., Nomura R., Yoshikawa Y.,

RA Matsumoto K., Hirano M., Sano S., Nomuyama H., Onogawa S.,

RA Kaeriyama S., Satoh N., Matsunawa H., Takahashi E., Kataoka R.,

RA Kuga N., Kuroda A., Satoh I., Kamata K., Takami S., Terashima Y.,

RA Kuga N., Kuroda A., Satoh I., Kamata K., Takami S., Terashima Y.,

RA Kuga N., Kuroda A., Satoh I., Kamata K., Takami S., Terashima Y.,

RA Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sato K., Nishikawa T.,

RA Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Kanehori K.,

RA Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;

Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.

DR GO; GO:0014936; F.hematopoietin/interferon-class (D200-domain. . .

DR GO; GO:004872; F:receptor activity; IEA.

DR InterPro; IPR0008957; FN_III-like.
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Best Local S
Matches 70
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Matches 63
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                                                                            GMVPPPENVRMNSVNFKNILQWESPAFAEG-NLTFTAQYLSYR----IFQDKCMNTTLTE
                                                                                                                           GGLPKPANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYFIYGQKKWLNKSECRNINRTY
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Primates;
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27, Last sequence update)
27, Last annotation update)
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Pred.
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Pred. No. 9.
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Catarrhini;
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                                                                                                                                                                                                          9.8e-13
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ЭТ.,
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RESULT 14
 [2]
SEQUENCE FROM N.A.
MEDLINE=96054036; PubMed=7563119;
Lutfalla G., McInnis M.G., Antonarakis
Lutfalla G., frhe human CRFB4 gene: com
                                                                                       Xie M.-H., Aggarwal S., Ho W.-H., Foster J., Zhang Z., Sti Wood W.I., Goddard A.D., Gurney A.L., Wood W.I., Goddard A.D., Gurney A.L., "Interleukin (IL)-22, a novel human cytokine that signals interferon receptor-related proteins CRF2-4 and IL-22R."; J. Biol. Chem. 275:31335-31339 (2000).

J. FUNCTION: Receptor for III10 and II22. Serves as an accessential for the active II10 receptor complex and to III10-induced signal transduction events.
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Q08334;
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                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=15340161; DOI=10.1110/ps.04682504; Zhang Z., Henzel W.J.; "Signal peptide prediction based on analy verified cleavage sites.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lutfalla G., McInnis M.(
"Structure of the human neighbor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=93300510; PubMed=8314576;

Lutfalla G., Gardiner K., Uze G.;

"A new member of the cytokine receptor

21 at less than 35 kb from IFNAR.";

Genomics 16:366-373(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Cytokine receptor CRF2-4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-FEB-1995 (Rel. 46, Last annotation update)
25-JAN-2005 (Rel. 46, Last annotation update)
Interleukin-10 receptor beta chain precursor (IL
(Cytokine receptor family 2 member 4) (Cytokine
                                                                                                                                                                                                                                                                                                                                MEDLINE=97459974; PubMed=9312047;
Kotenko S.V., Krause C.D., Izotova
This SWISS-PROT entry is copyright. between the Swiss Institute of Bioi
                                           -!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SIMILARITY: Belongs to the type II cytokine family o
-!- SIMILARITY: Contains 2 fibronectin type III domains.
                                                                                                                                                                                                       MEDLINE=20469498; PubMed=10875937; DOI=10.1074/jbc.M005304200;
Xie M.-H., Aggarwal S., Ho W.-H., Foster J., Zhang Z., Stinson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 20-34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Fetal brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=IL10RB;
                                                                                                                                                                                                                                      CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                "Identification and functional characterization
                                                                                                                                                                                                                                                                                                                Pestka S.;
                                                                                                                                                                                                                                                                                                                               Kotenko S.V., Krause
                                                                                                                                                                                                                                                                                                                                                                 CHARACTERIZATION.
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                                                                                                                                                                                                                                                                   interleukin-10 receptor complex.";
) J. 16:5894-5903(1997).
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                                                                                                                                                                                                                                                                                                                                  Izotova
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   Bioinformatics
                                                                                                                                                                                                                                                                                                                               DOI=10.1093/emboj/16.19
a L.S., Pollack B.P., Wu
                                                                                                                                                                                                                                                                                                                                                                                                                             analysis
    It is produced through a collaboration -
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GO; GO:0016021; C:intey...
GO; GO:00016021; C:plasma membrane; ...
GO; GO:0004920; F:interleukin-10 receptor activity; TAS.
GO; GO:0004972; F:receptor activity; TAS.
GO; GO:0006955; F:immune response; TAS.
GO; GO:0006954; F:inflammatory response; TAS.
GO; GO:0006954; F:inflammatory response; TAS.
GO; GO:000165; F:signal transduction; TAS.
InterPro; IPR000282; Cytok receptor_2.
InterPro; IPR001187; FN_III_-like.
R InterPro; IPR001187; Tissue factor.
R Pfam; PF01108; Tissue fac; I.
R Pfam; PF01108; Tissue fac; I.
M Direct protein sequencing; Glycoprotein; Rece
M Direct protein sequencing; Glycoprotein; Rece
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Best Local S
Matches 63
                  Q9BUU4;
Q9BUU4;
01-JUN-2001
01-JUN-2001
25-OCT-2004
Interleukin
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H-InvDB; HIX0016074; -
MIM; 123889; -
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EMBL; U08988; AAA86872.1;
PIR; A47003; A47003.
HSSP; P13726; ITFH.
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                                                                                                                                                                                                                                       EPWTTYCVQVRGFLPDRNKAGEWSEPVCEQTTHDET
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166
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1151
1124
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274
                    (TrEMBLrel. 17, Created)
(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 28, Last annotation updat
10 receptor, beta,.
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                                                                                                                               PRELIMINARY;
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FLGHP -> VGRME (in Ref. 2).

Missing (in Ref. 2).

M; 66706C79F8514B23 CRC64;
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Potential.
Cytoplasmic (Potential).
Fibronectin type-III.
By similarity.
By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 232.5; DB 1;
Pred. No. 1.2e-12;
6; Mismatches 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-linked
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d (GleNAc...)
d (GleNAc...)
d (GleNAc...)
                                                                                                                               325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) receptor beta (Potential).
                                        update)
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(Potential).
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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA RA S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J. W., Green B.J., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.B., Schmerch A., Schein J.B.,
RA Genes S.J., Marra M.A.;
                                                                                                                    Matches
                                                                                                                                  Query Match
Best Local (
                                                                                                                                                                               Receptor.
SEQUENCE
                                                                                                                                                                                                                                         InterPro;
InterPro;
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Submitted (AUG-2003) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUB=Kidney;
Strausberg R.;
Submitted (JAN-2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rieder M.J., Carrington
Ahearn M.O., Kuldanek S.
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MEDLINE=22388257;
                                                                                                                                                                                                            SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Koundinya M., Raphael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kalnine N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Generation and initial analysis of more than 15,000
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                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                       P; P13726; ITFH.
GO:0016021; C:integral to membrane; IEA.
GO:0004896; F:hematopoietin/interferon-class (D200-domain. .
GO:0004872; F:receptor activity; IEA.
GO:0007596; F:blood coagulation; IEA.
GO:0007596; F:blood coagulation; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mouse cDNA sequences.";
c. Natl. Acad. Sci. U.S.
                                                                                                                                                                                                                                                                                                                                                                            BC001903; AAH01903.1; -. AY323826; AAP72016.1; -. BT009777; AAP88779.1; -.
74
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                                                                                                                                                                                                            SM00060;
                                                                                                                                  Similarity
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); IPR003961; PN III.

); IPR008957; FN III-11ke.

); IPR001187; Tissue factor

01108; Tissue_fac; I.
                          CDLSAETSDYEHQYYAKVKAIWGTKCSKWAESGRFYPFLETQIGPPEVALTTDEKSISVV
                                                       GMVPPPENVRMNSVNFKNILOWESPAFAKG-NLTFTAQYLSYR----IFQDKCMNTTLTE
                                                                          GGLPKPANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYFIYGQKKWLNKSECRNINRTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FROM N.A.
CDFSSLSKYGDHT---LRVRAEFADEHSDWVNI-TFCPVDDTIIGPPGMQVEVLADSLHMR
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(JUN-2003)
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                                                                                                                    Conservative
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Primates;
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29.2%;
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